SEARCH REQUEST FORM

7.511

Requestor's Name: Name: Name: Serial Number: 09/047,652 Date: 7-2098 Phone: 305-5860 Art Unit: 1642
Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).
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Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

MasPar time 828.83 Seconds 1312.667 Million cell updates/sec Tue Jul 21 14:53:17 1998; Run on:

not generated. output Tabular

>US-09-047-652A-1 (1-652) from US09047652A.seq 652

.....GITCTIGGAACAIGGAATIT CCACGCGAAGGTCTCCGCT.. Title: Description: Perfect Score: N.A. Sequence: Comp:

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default TABLE Gap 6 table: Scoring

Query 0 Dbase 0; STD Nmatch 457396 segs, 834342348 bases Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

emb154 Database:

Database:

1:em_ba 2:em_htg 3:em_huml 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_vi genbank106 13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat 19:gb_ph 20:gb_pl 21:gb_prl 22:gb_pr2 23:gb_ro 24:gb_st 25:gb_sy 26:gb_un 27:gb_vi

Variance 5.497; scale 1.888 Mean 10.377; Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Direct Submission
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	31328 Labege Cedex, France
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Direct Submission
Submitted (23-MAR-1998) Wellcome Trust Genome
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonered
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/clone="119182"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 2080 to 3683)
Yakovlev, A.G., Ruffo, M., Jurka, J. and Krueger, K.E.
Comparison of repetitive elements in the third intron crodent mitochondrial benzodiazepine receptor-encoding gene 155 (2), 201-205 (1995)
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2 (bases 1 to 4258)
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/product-"mitochondrial k
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Georgetown University School o
Location/Qualifiers
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/note="4 Alus"
/rpt_family="Alu"
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/db_xref*"PID:g163489"
/translation="MAPPWVPAVGFTLLPSLGGFLGAQYTRGEGFRWYASLQKPPWHPPRWILAPIWGTLYSAMGYGSYMIWKELGGFSKEAVVPLGLYAGOLALNWAWPPLFFGTROMGWALVDLLLTGGMAAATAMAWHQVSPPAACLLYPYLAWLAFAGMLNYRMWQDNQVRRSGRRLSE"
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M64520
g163488
benzodiazepine receptor isoquinoline binding protein.
Calf adrenal gland, cDNA to mRNA.
Bos taurus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 821)
Parola, A.L., Stump, D.G., Pepper, D.J., Krueger, K.E., Rega Laird, H.E.II.
Cloning and expression of a pharmacologically unique bov peripheral-type benzodiazepine receptor isoquinoline bin
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Pred. No. 1.44e-196;
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Russell'
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/codon_start=1
/product="benzodiazepine r
protein"
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                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/dev_stage="calf"
/tissue_type="adrenal g
/tissue_lib="of David F
67. .806
                                                                                                                                                                                                                                                            Chem. 266, 14082-14087
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1. .821
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/gene="PBR/IBP"
67. .576
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/gene="PBR/IBP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                /product="peripheral-type benzodiazepine receptor"
/db_xref="PID:g309442"
/translation="MPESWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHP
PRWTLAPIWGTLYSAMGYGSYIVWKELGGFTEDAMVPLGLYTGQLALNWAWPPIFFGA
RQMGWALADLLLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATVLNYYVWRDNSG
RRGGSRLPE"
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                                                                                                                                                                                                                                                          to 626)
Dimchev, A.B., Boujrad, N., Price, J.M., Musto, N.A.
                                         TGCCGGCATGCTCAACTACCGCATGTGGCAGGACAACCAGGTCCGGAGGAGTGGCCGGCG
GGCGAGGGCCTCCGGTGGTATGCTAGCTTGCAGAAACCCTCTTGGCATCCGCCTCGCTGG
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                                                                                                                                                                                                                             ; Chordata;
Myomorpha;
                                                                                                                                                                                                                                                           1 (bases 1 to 626)
Garnier, M., Dimchev, A.B., Boujrad, N., Price, J.M., Musto Papadopoulos, V.
In vitro reconstitution of a functional peripheral-type benzodiazepine receptor from mouse Leydig tumor cells Mol. Pharmacol. 45 (2), 201-211 (1994)
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                                                                                                                                                               mRNA,
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                                                                                     607
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Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                receptor
                                                                                                                                                                                                         mRNA
                                                                                                                                                      ROD
                                                                                   tumor"
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l. No. 8.06e-192;
Mismatches 91;
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                                                                                                                                              MUSMPBR 626 bp mRNA
Mouse peripheral-type benzodiazepine
L17306
g309441
benzodiazepine receptor.
Mus musculus mouse testis tumor cDNA
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/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="MA-10"
/cell_type="leydig"
/tissue_type="mouse testi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 282;
Pred. No. 8
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/codon_start=1
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larity 80.4%;
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35. .544
/note="peripheral-type benzodiazepine receptor"
/codon_start=1
/db_xref="PID:g206162"
/translation="MSQSWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHP
PRWTLAPIWGTLYSAMGYGSYIIWKELGGFTEEAMVPLGLYTGQLALNWAWPPIFFGA
RQMGWALVDLMLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATMLNYYVWRDNSG
RRGGSRLTE"
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mRNA, COMP
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CTGGCTTTTGCC
            CAGGTGAGCCCGCTGGCCGCCTGCTCTACCCCTACCTGGCCTGGCTGACG
                                                    ACCGTGCTCAACTACTATGTATGGCGCGATAACTCTGGCCGGCGAGGGGGCTCCCGGCTC
                                                                 TGGAAAGAGCTGGGAGGTTTCACAGAGGAGGCTATGGTTCCCTTGGGTCTCTACACTGGT
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpl
Murinae; Rattus.

1 (bases 1 to 781)
Sprengel,R., Werner,P., Seeburg,P.H., Mukhin,A.G., Sal
Grayson,D.R., Guidotti,A. and Krueger,K.E.
Molecular cloning and expression of cDNA encoding a pubenzodiazepine receptor
J. Biol. Chem. 264, 20415-20421 (1989)
90062173
Draft entry and computer readable copy of sequence [1]
provided by Krueger,K.E., 20-SEP-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                781;
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                                                                                                                                                                                                       (PKBS)
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  CITGCTGTACCCTTACCTGGCCTGG
                                                                                                                                    468
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                                                                                                       CCAGAGTGAAGGCACCCAGCCATCAGGAATGCAGCCTGCCAGC
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                                                                                                                                                                                                                                                          receptor to mRNA.
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/organism="Rattus norvegicus/db_xref="taxon:10116"
35. .544
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                                                                                                                                                                                         benzodiazepine
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Rat peripheral-type benzodiazepi
cds.
J05122
9206161
peripheral-type benzodiazepine re
Rat adult adrenal cortex, cDNA to
Rattus norvegicus
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353; Conservative
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/codon_start=1
/product="peripheral-type benzodlazepine receptor"
/db_xref="piD:d1005281"
/db_xref="PiD:g484054"
/db_xref="PiD:g684054"
/db_xref=
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1 (bases: 1 to 856)

Taketani, S., Kohno, H., Okuda, M., Furukawa, T. and Tokunaga, R. Induction of peripheral-type benzodiazepine receptors during differentiation of mouse erythroleukemia cells. A possible involvement of these receptors in heme biosynthesis juvolvement of the 269, 2527-7531 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDBJ/EMBL/GenBank databases. rsity, Dept. of Hygiene; 10-15
                                                                                                          GCCTTGGTGGATCTCCTGCTGGTCAGTGGGGGGGGGGGCGCACTACCGTGGCCTGGTAC
                                                                                                                                                                                                                                                                                                            Mouse mRNA for peripheral-type benzodiazepine receptor, D21207
g484053
                                                                                                                                                                                                                                                                                                                                                                                                                    lambda
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Pred. No. 1.71e-185; 0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                               peripheral-type benzodiazepine receptor
Mus musculus cell-line erythroleukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="erythroleukemia"
/clone_lib="lambda gtil"
66. .575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-992-1001 x2504
06-992-3522.
Location/Qualifiers
1. .856
/organism="Mus muscu:
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                       mRNA
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larity 79.5%;
Conservative
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AUTHORS
TITLE
JOURNAL
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tissues
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Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.
The human peripheral benzodiazepine receptor gene: cloncharacterization of alternative splicing in normal tissipatient with congenital lipoid adrenal hyperplasia Genomics 18, 643-650 (1993)
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g483404
benzodiazepine receptor; peripheral benzodiazepine
3 of 4
Homo sapiens DNA
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138 t
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Pred. No. 6.34e-72;
0; Mismatches 0
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1. .645
/organism-"Homo sapiens"
/db_xref-"taxon:9606"
/tissue_type="placenta"
/tissue_lib-"placenta"
224. .362
/product-"peripheral benz
a 177 c 192 g 138
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larity 98.6%;
Conservative
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Homo sapiens
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Issues
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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 487)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
/tissue_lib="placenta"
/tissue_lib="placenta"
/fissue_lib="placenta"
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                                                                                                                                                         benzodiazepine receptor
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1. No. 2.10e-55
Mismatches
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                                                                                                                                      HSPBR2 487 bp DNA
Human peripheral benzodiazepine rect
L21952
g483403
benzodiazepine receptor; peripheral
2 of 4
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Unknown.

Unclassified.

1 (bases 1 to 7218)

Dorner, F., Scheiflinger, F. and Fa
Recombinant fowlpox virus
Recombinant fowlpox virus

Location/Qualifiers

1. .7218

1. .7218

1486 g 1'
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/product="peripheral-type benzodiazepine receptor"
/db_xref="PID:9206480"
/translation="MSQSWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHPPRWTLAPIWGTLYSAMGYGSYIIWKELGGFTEEAMVPLGLYTGQLALNWAWPPIFFGARGMALVDLMLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATMLNYYVWRDNSGRRGGSRLTE"
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2 of 2
Rattus norvegicus (strain Wistar) Adult DNA.
Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Nurinae; Rattus.

1 (bases 1 to 3434)
                                                                                             ROD
                                                                                                          receptor
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Casalotti,S.O., Pelaia,G., Yakovlev,A.G.,
and Krueger,K.E.
Structure of the rat gene encoding the mit
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Pred. No. 3.97e-62;
0; Mismatches 13;
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/strain-"Wistar"
/db_xref-"taxon:10116"
/dev_stage-"adult"
order(M95864:1273. .1462,1. .1
                                                                                                                                                                                                                                                                                                                                                                                                       Bam HI
                                                                            RATPTBZR02 3434 bp DNA
Rat peripheral-type benzodiazepine
complete cds.
M84221
g206478
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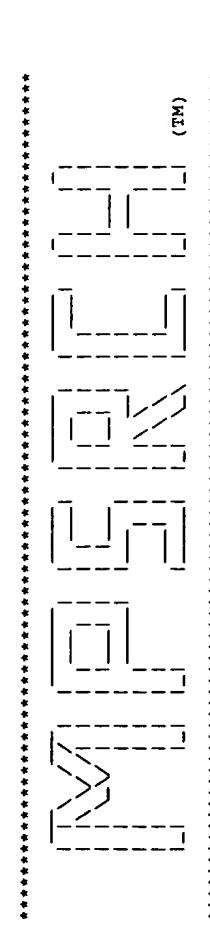
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receptor (MBR)
                                                                   72
                Gaps
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                                         TCTCCGCTGGTACGCCGGCCTGCAGAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGG
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                                                                                                                                                                                                                                                                  /evidence=experimental
/product="mitochondrial benzodiazepine receptor"
join(<1. .40,1030. .>1084)
/gene="MBR"
/codon_start=2
/product="mitochondrial benzodiazepine receptor"
/db_xref="PID:91039378"
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Myomorpha;
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Yakovlev,A.G., Ruffo,M., Jurka,J. and Krueger,K.E.
Comparison of repetitive elements in the third intron of rodent mitochondrial benzodiazepine receptor-encoding ger Gene 155 (2), 201-205 (1995)
95237610
2 (bases 1 to 1084)
Krueger,K.E.
Direct Submission
Submitted (19-JUL-1994) Karl E. Krueger, Dept. of Cell Bi Georgetown University School of Medicine, Washington, DC Location/Qualifiers
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               Indels
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Cricetulus griseus mitochondrial benzodiazepine
gene, partial cds.
U12420
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Cricetulus griseus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; I
Cricetinae; Cricetulus.
1 (bases 41 to 1029)
 Pred. No. 1.82e-08; 203; Mismatches 165;
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/organism="Cricetulus griseus"
/db_xref="taxon:10029"
/clone_lib="PCR of genomic DNA/cell_line="V79"
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/gene="MBR"
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Pred. No. 3.04e-07
0; Mismatches
                                              /evidence-experimental
162. .300
/rpt_family="B1"
340. .422
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657. .736
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1030. .>1084
/gene="MBR"
        41. .1029
/gene="MBR"
/number=3
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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.....GTTCTTGGAACATGGAATTT >US-09-047-652A-2 (1-652) from US09047652A.seq 652 CCACGGCGAGGGTCTCCGCT. -1 Title:
Description:
Perfect Score:
N.A. Sequence:
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default TABLE Gap 6 Scoring table:

Query 0 Dbase 0; STD Nmatch

~ × 457396 seqs, 834342348 bases Searched

summaries Minimum Match 0% Listing first 45 Post-processing:

emb154 Database:

1:em_ba 2:em_htg 3:em_huml 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_v1 genbank106
13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_l 19:gb_ph 20:gb_pl 21:gb_pr1 22:gb_pr2 23:gb_ro 24:gb_25:gb_sy 26:gb_un 27:gb_v1 Database:

18:gb_pat o 24:gb_st

scale 1.885 Variance 5.505; Mean 10.376; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	7	σ	4	2	16.	BOVPBRIBP	Calf peripheral-type b	.45e-19
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ď	1.26e-06	.97e-	.79e-	2.79e-04	.73e+	.73e+	.73e+	.73e+	.73e+	.73e+	1.73e+00	.736+	.73e+	.49e+	.49e+	.49e+	.49e+	.49e+	.49e+	.49e+0	.49e+0	9.	9.	.69e+0	.69e+0	1.69e+01	φ.	.69e+0	1.69e+01
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ALIGNMENTS

HUMHPBS 821 bp mRNA PRI 20-DEC-1993 Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds. g184333 peripheral benzodiazepine receptor. Human cDNA to mRNA. Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	to 821) to 821) attei, M.G., Kaghad, M., Dumont, X., Guillemot, ut, D. and Ferrara, P. loning and chromosomal localization of a hum type benzodiazepine receptor chem. 195 (2), 305-311 (1991) to 821)	Nicona, J. Direct Submission Direct Submission Submitted (27-JUN-1990) J. Riond, Sanofi Elf Bio-Recherches, BP137, 31328 Labege Cedex, France Location/Qualifiers 1. 821 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_line="hystiocytic lymphoma monocyte-like cell line U937" /clone="p-hpBS11"	<pre><1811 /note="peripheral benzodiazepine receptor mRNA" 62571 /note="peripheral benzodiazepine receptor" /codon_start=1 /db_xref="PID:9306883" /translation="MAPPWVPAMGFTLAPSLGCFVGSRFVHGEGLRWYAGLOKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYTGQLALNWAWPPIFFGARWHGGRRLPE"</pre> WHGGRRLPE"
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1 Lin, D., Chang, Y.J., Strauss, J.F. and Miller, W.L.
The human peripheral benzodiazepine receptor gene: cloning characterization of alternative splicing in normal tissues patient with congenital lipoid adrenal hyperplasia
Genomics 18 (3), 643-650 (1993)
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PLPGLAGLRDHTQLLRMAGQPWLAWGTAAARVSARPTRDCSCTSRCHHACDVVAVTLS
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Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.

Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.

The human peripheral benzodiazepine receptor gene: clon
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/codon_start=1
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Direct Submission
Submitted (23-MAR-1998) Wellcome Trust Genome
Cambridgeshire, CB10 1SA, UK. E-mail enquires
humquery@sanger.ac.uk Clone requests: clonered
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                                                          /db_xref="taxon:9606"
/tissue_type="placenta"
/tissue_lib="placenta"
join(L21952:195. .376, L21
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Primates; Catarrhini; Hominidae;
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characterization of alternative patient with congenital lipoid a Genomics 18, 643-650 (1993) 94140364
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Human DNA sequence *

1191B2; HTGS phase 1

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HTG; HTGS_PHASE1.

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IMPORTANT: This sequence is unimizated and does not necessarily important; This sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of sequence: bkill9182 Contig_ID: 01607 acc Length: 2099 bu Infinished sequence: bkill9182 Contig_ID: 01607 acc Length: 2099 bu Infinished sequence: bkill9182 Contig_ID: 01607 acc Length: 1033 bp Unfinished sequence: bkill9182 Contig_ID: 01606 acc Length: 1183 bp Unfinished sequence: bkill9182 Contig_ID: 01606 acc Length: 1183 bp Unfinished sequence: bkill9182 Contig_ID: 00046 acc Length: 1183 bp Unfinished sequence: bkill9182 Contig_ID: 00046 acc Length: 20053 acc Length: 20053 acc Length: 20053 acc Length: 20055 acc L
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
/clone="119182"
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/product="mitochondrial benzodiazepine receptor"
/db_xref="PID:g529946"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordat
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 2080 to 3683)
Yakovlev, A.G., Ruffo, M., Jurka, J. and Krueger, K.E.
Comparison of repetitive elements in the third intron
rodent mitochondrial benzodiazepine receptor-encoding
Gene 155 (2), 201-205 (1995)
95237610
2 (bases 1 to 4258)
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Medicine, Washington,
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/product-"mitochondrial b
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/note="4 Alus"
/rpt_family="Alu"
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/gene="MBR"
join(129. .310,1941.
/gene="MBR"
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Krueger, K.E.
Direct Submission
Submitted (19-JUL-1994) Karl E
Georgetown University School o
Location/Qualifiers
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/gene="MBR"
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/gene="MBR"
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1 (bases 1 to 1020000)

Buck, D.

Buck, D.

Direct Submission

Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Cambridgeshire, CB10 1SA, UK. E-mail enquires:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

IMPORTANT: This sequence is unfinished and does not necessarily

IMPORTANT: This sequence is unfinished and does not necessarily

represent the correct sequence. Work on the sequence is in progress

"he sequence may be
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Human DNA sequence ***

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HTG; HTGS_PHASE1.
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Location/Qualifiers

1. 152843

/organism="Homo sapiens
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                                                                                                                                 ; Metazoa; Ruminantia;
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                                                                  receptor
                                                                                                                                                                                                                                                                                                                                                       receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 290; DB 16;
Pred. No. 7.45e-198;
0; Mismatches 80;
                                                    BOVPBRIBP 821 bp mRNA
Calf peripheral-type benzodiazepine rec
protein (PBR/IBP) mRNA, complete cds.
M64520
g163488
benzodiazepine receptor isoquinoline bi
Calf adrenal gland, cDNA to mRNA.
Bos taurus
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                                                                                                                              Eukaryotae; mitochondrial eukaryotes;
Vertebrata; Eutheria; Artiodactyla; I
Bovidae; Bovinae; Bos.
1 (bases 1 to 821)
Parola, A.L., Stump, D.G., Pepper, D.J.
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/product="benzodiazepine
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/gene="PBR/IBP"
67. .576
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'gene="PBR/IBP"
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/gene<del>-</del>"PBR/IBP
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Similarity 82.3%;
382; Conservative
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/db_xref="PID:9309442"
/translation="MPESWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSV
PRWTLAPIWGTLYSAMGYGSYIVWKELGGFTEDAMVPLGLYTGQLALNWAWPPIFN
RQMGWALADLLLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATVLNYYVWRDN
RRGGSRLPE"
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A, complete
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Garnier, M., Dimchev, A.B., Boujrad, N., Price, J.M., Musto, N.A.
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                                                 TGCCGGCATGCTCAACTACCGCATGTGGCAGGACAACCAGGTCCGGAGGAGTGGCCGGCG
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Myomorpha;
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In vitro reconstitution of a functional peripheral-type benzodiazepine receptor from mouse Leydig tumor cells Mol. Pharmacol. 45 (2), 201-211 (1994) 94158796
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Sciurognathi;
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                                                                                                                                              receptor
                                                                                                                                                                                      to mRNA
                                                                                                                                       ROD
                                                                           Score 284; DB 23;
Pred. No. 4.13e-193;
0; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                tumor
                                                                                                                       Mouse peripheral-type benzodiazepine re L17306 g309441 benzodiazepine receptor.
Mus musculus mouse testis tumor cDNA to Eukarunt-
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/db_xref="taxon:10090"
/cell_line="MA-10"
/cell_type="leydig"
/tissue_type="mouse testi
                                                                                                                                                                                                        Eukaryotae, mitochondrial eukar
Vertebrata; Eutheria; Rodentia;
Murinae; Mus.
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Similarity 80.6%;
374; Conservative
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/codon_start=1
/db_xref="PID:g206162"
/translation="MSQSWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHP
PRWTLAPIWGTLYSAMGYGSYIIWKELGGFTEEAMVPLGLYTGQLALNWAWPPIFFGA
RQMGWALVDLMLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATMLNYYVWRDNSG
RRGGSRLTE"
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ACCGTGCTCAACTACTATGTATGCGCGCGATAACTCTGGCCGGCGGCGGGGGGCTCCCGGCTC
                                                                      Myomorpha;
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Sprengel, R., Werner, P., Seeburg, P.H., Mukhin, A.G., Grayson, D.R., Guidotti, A. and Krueger, K.E.
Molecular cloning and expression of cDNA encoding a benzodiazepine receptor
J. Biol. Chem. 264, 20415-20421 (1989)
Draft entry and computer resident
                                                                                                                                                                                                           (PKBS)
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Rat adult adrenal cortex, cDNA to mRNA.
Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
                                                                                                                                          468
                                                                                                              575
                                                                                                                                                                                                 mRNA ROD benzodiazepine receptor
                                                                                                               CCAGAGTGAAGGCACCCAGCCATCAGGAATGCAGCCTGCCAGC
                                                                                                                             e 278; DB 23;
. No. 2.27e-188;
Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Draft entry and computer readable copy of provided by Krueger, K.E., 20-SEP-1989.
Location/Qualifiers
1. .781
/organism="Rattus norvegicus"/db_xref="taxon:10116"
35. .544
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Pred. No. 2
0; Mismat
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Similarity 82.3%;
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/codon_start=1
/product="peripheral-type benzodiazepine receptor"
/db_xref="PID:d1005281"
/db_xref="PID:g484054"
/db_xref="PID:g484054"
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2 (bases 1 to 856)

5 Taketani, S.

Direct Submission

L. Submitted (15-OCT-1993) to the DDBJ/EMBL/GenBank databases. Shig Taketani, Kansai Medical University, Dept. of Hygiene; 10-15

Fumizono-cho, Moriguchi, Osaka 570, Japan

(Tel:06-992-1001(ex.2504), Fax:06-992-3522)

Submitted (15-Oct-1993) to DDBJ by:

Shigeru Taketani

Depertment of Hygiene

Kansai Medical University

1-Fumizonocho, Moriguchi
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                       GCCTTGGTGGATCTCCTGCTGGTCAGTGGGGCGGCGGCAGCCACTACCGTGGCCTGGTAC
                                                                              ACCATGCTCAACTACTATGTATGGCGTGATAACTCTGGTCGGCGAGGGGGCTCCCGGCTC
                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.

1 (bases 1 to 856)
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                                                                                                                                                                                                              MUSPTBR 856 bp mRNA ROD 27-MAI MOUSE mRNA for peripheral-type benzodiazepine receptor,
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1. No. 8.60e-187;
Mismatches 94;
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peripheral-type benzodiazepine receptor
Mus musculus cell-line erythroleukemia
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/db_xref="taxon:10090"
/cell_line="erythroleukemia
/clone_lib="lambda gtll"
66. .575
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06-992-3522.
Location/Qualifiers
1. 856
/organism="Mus muscu./strain="BALB/c"
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Best Local Similarity 79.7%;
Matches 370; Conservative
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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)
Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.
The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and patient with congenital lipoid adrenal hyperplasia
Genomics 18, 643-650 (1993)
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Pred. No. 8.17e-72
0; Mismatches
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1. .645
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
/tissue_lib="placenta"
224. .362
/product="peripheral benz
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/codon_start=1
/product="peripheral-type benzodiazepine receptor"
/db_xref="PID:g206480"
/translation="MSOSWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHPPRWTLAPIWGTLYSAMGYGSYIIWKELGGFTEEAMVPLGLYTGOLALNWAWPPIFFGARGMGALVDLMLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATMLNYYVWRDNSGRRGGSRLTE"
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1 (bases 1 to 3434)
Sprengel,R., Werner,P., Seeburg,P.H., Mukhin,A.G., Sargrayson,D.R., Guidotti,A. and Krueger,K.E.
Molecular Cloning and Expression of cDNA Encoding a Pagenzodiazepine Receptor
J. Biol. Chem. 264, 20415-20421 (1989)
90062173
2 (bases 1 to 3434)
Casalotti,S.O., Pelaia,G., Yakovlev,A.G., Csikos,T., and Krueger,K.E.
Structure of the rat gene encoding the mitochondrial receptor
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Vertebrata; Eutheria; Rodentia; Sciurognathi;
Murinae; Rattus.
                                                                       RATPTBZR02 3434 bp DNA
Rat peripheral-type benzodiazepine receptor
complete cds.
M84221
g206478
                                                                                                                                                                   norvegicus (strain Wistar) Adult DNA
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Pred. No. 4.95e-62;
0; Mismatches 13;
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93077057
Sequence M84221 start.
7kb between sequences.
1. .3434
/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
/dev_stage="adult"
order(M95864:1273. .1462,1. .1
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Rattus norvegicus
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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordat
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 487)
Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.
The human peripheral benzodiazepine receptor gene: cla
characterization of alternative splicing in normal tis
patient with congenital lipoid adrenal hyperplasia
Genomics 18, 643-650 (1993)
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| Mismatches 0
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Dorner, F., Scheiflinger, F. and Falki
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997
Location/Qualifiers
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1. .487
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
/tissue_lib="placenta"
166. .376
/product="peripheral benz
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Search completed: Tue Jul 21 15:51:40 1998 Job time : 845 secs.
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(MBR)
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gene, partial cds.
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9529943
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                                    TCTCCGCTGGTACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGG
                                                                                    CCTGTCTGGGGCACGCTCTACTCAGCCATGGGGTACGGCTCCTACCTGGTCTGGAAAGA
                                                                                                                                                   CTGGGAGGCTTCACAGAGAGGCTGTGGTTCCCCTGGGCCTCTACACTGGGCAGCTGGC
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/product="mitochondrial benzodiazepine receptor"
join(<1. .40,1030. .>1084)
/gene="MBR"
/codon_start=2
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/db_xref="PID:g1039378"
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Yakovlev, A.G., Ruffo, M., Jurka, J. and Krueger, K.E.
Comparison of repetitive elements in the third intron
rodent mitochondrial benzodiazepine receptor-encoding
Gene 155 (2), 201-205 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chinese hamster.
Cricetulus griseus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutherla; Rodentia; Sciurognathi; l
Cricetinae; Cricetulus.
Cricetinae; Cricetulus.
'hases 41 to 1029)
'hases 41 to 1029)
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of Medicine,
. No. 1.90e-08;
Mismatches 165;
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/db_xref="taxon:10029"
/clone_lib="PCR of genomic DNA"
/cell_line="V79"
1. .1084
/gene="MBR"
<1. .40
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/gene="MBR"
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Gaps
                                                   / widence-experimental
162. .300
/rpt_family-"B1"
340. .422
/rpt_family-"Alu-like"
657. .736
/rpt_family-"B1"
1030. .>1084
/gene="MBR"
/number=4
/evidence-experimental
/product="mitochondrial benzodiazepine receptor"
3 a 279 c 302 g 250 t
/translation-"WPPIFFGARQMGWALADLLLVSGVATATTLA
41. .1029
/gene-"MBR"
/number-3
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                                                                                                                                                                                                                                                   Length 1084
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Pred. No. 3.15e-07
0; Mismatches
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Best Local Similarity 95.1%;
Matches 39; Conservative
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Unit. Research . Collins, Biocomputing Research 1998 University of Edinburgh, U n rights by Oxford Molecular Ltd Release 3.1A John F. Copyright (c) 1993-19 Distribution

Smith-Waterman search, database MPsrch_nn

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algorithm

MasPar time 108.29 Seconds 766.833 Million cell updates/sec Tue Run

21 15:25:04 1998 Jul 0

generated not output Tabular

..GTTCTTGGAACATGGAATTT CCACGGCGAAGGTCTCCGCT.. sed >US-09-047-652A-1 (1-652) from US09047652A 652 ~ Title:
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Comp:

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~ bases 63680241 seds, 176886 Searched

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n-geneseg31-2 l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37

scale 1.565 5.444; Variance 8.518; Mean Statistics

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Ø Pred. score and 18

SUMMARIE

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Res		core	Query Match	Length	DB		ipt	Pred. No.
	1		36.5	(20	2219	Human gene signature	.02e-1
O	7		•	91	σ	5174		2.23e-11
U	ო		•	204	Н	8116	ase substituted	.04e-0
	マ		•	91	δ	5174	1gonucl	.68e-0
U	ហ		•		12	7046	neric DNA sequ	.38e-0
	9		•	204		8116	Base substituted E.co	.38e-0
	7		•	┥		7046	Generic DNA sequence	.83e-0
	ထ		•			7046	Generic DNA sequence	.18e-0
	თ		•			7047	Generic DNA sequence	.18e-0
			•	114		7046	Generic DNA sequence	.18e-0
	11	34	5.2	114	12	070467	Ŋ	ŧ
U	12		•	114		7046	Generic DNA sequence	.18e-0
U			•	114		7046	DNA S	.18e-0
U	14		•	114		7046	Generic DNA sequence	.06e-0

6.81e-05 6.81e-05 6.81e-05	.81e-0	.22e-0	7.17e-04 7.17e-04	.17e-0	.28e-	ė	. 28e-	.17e-0	.17e-	7		7	6.77e-02	6.77e-02	.77e-	.77e-	6.77e-02	2.03e-01	ė	2.03e-01	2.03e-01	5.96e-01	5.96e-01	5.96e-01	5.96e-01	5.96e-01
Generic DNA sequence Generic DNA sequence	n endothelin-1	uman interleukin 8	Generic DNA sequence	hymase antisense o	eneric DNA s	Generic DNA sequence	MDNCF an	Generic DNA sequence	Human IL6 antisense o	Ŧ	44	HCV envelope region n	ntise	Human endothelin ETA	tisense	Chymase antisense ol1	Inducible nitric oxid	Human RANTES antisens	uman MDNC	Substance P antisense	Substance P antisense	Human IL4 antisense o	AR library	Human vascular cell a	Human defensin 1 anti	Substance P receptor
Q70466 Q70470 T76405	7640	7636	7047 7046	7645	7047	7047	7627	7047	7623	7047	7636	3507	7621	7642	7623	7645	7652	7630	627	7643	T76438	7618	61	15	T76294	44
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ALIGNMENTS

Claim 1; Page 1068; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. Couble-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

C sequence 272 BP; 43 A; 78 C; 86 G; 51 T; e.9 frequency; detection; 3'-directed human cDNA library - function, by preparing cDNA that corresp. mRNA in specific human SSULT 1
T22195 standard; cDNA to mRNA; 272 BP.
T22195;
T22195;
T22195;
Human gene signature HUMGS03766.
Gene signature; messenger RNA; mRNA; relative abundance; fre human; cloning; mapping; non-biased library; diagnosis; determine sapiens.
Homo sapiens.
Homo sapiens.
W09514772-Al.
Ol-JUN-1995.
Il-NOV-1994; J01916.
F 11-NOV-1993; JP-355504.
A (MATS/) MATSUBARA K.
A (OKUB/) OKUBO K. Matsubara K, Okubo K; WPI; 95-206931/27. Identifying gene signatures in for diagnosis of abnormal cell reflects relative abundance of RESULT

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Earlosure; p; English.

Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                          vhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv
                                                                                                   completion of molecules
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by prepn of single stranded template,
misincorporation, completion of molecu
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larity 7.7%;
Conservative
        EP-285123-A.
05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, K
/*tag=
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Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of Oligonucleotide probe MK14-A consists of nucleotides 5-95 of Oligonucleotide probe MK14-A consists of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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N81164;
N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
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EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria - u detection and amplification of Mycobacteria nucleic acid
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          e 238; DB 20; L
|. No. 3.02e-134;
| Mismatches 20;
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/*tag= a
/function=multiple cloning
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TGGCCGTCACGCTTTCATGACCACTGGGCCTG
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            Score
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0; M
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           Match 36.5%;
Local Similarity 92.3%;
nes 251; Conservative
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e 41; DB 1; Le. No. 1.04e-09; Mismatches 35;

Score 41; Pred. No.

Pred. 60;

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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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Synthetic.

Synthetic.

EP-571911-A.

01-DEC-1993.

24-MAY-1993; 108325.

R 26-MAY-1992; US-889651.

A (BECT ) BECTON DICKINSON CO.

I Shank DD, Spears PA;

WPI; 93-378844/48.

WPI; 93-378844/48.

The wollgo:nucleotide probes specific for Mycobacteria acid

A that ion and amplification of Mycobacteria nucleic acid

Antection and amplification of Mycobacteria nucleic acid
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87
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
42; Mism
                                                                             BP
                                                                                                                                 Y-
                                                     O51746 standard; cDNA; 91 BF
Q51746;
31-MAY-1994 (first entry)
Oligonucleotide probe MK14-P
Oligonucleotide; DNA probe;
                                                                                                                                               DNA probe;
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col1

Escherichia

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in
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                             Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding dom effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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39 (see
                                                                                         uence represents 'Z
or 12 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                             )7;
74;
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|. No. 5.38e-07;
| Mismatches 74
                                                                                         sequence
5, 9 or 12
                                                                Location/Qualifiers
55..60
/*tag= a
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Pred.
33; N
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                                                                                                                 01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KBY BK:
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"this
        ВР
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N81164;
O8-NOV-1990 (first entry)
Base substituted E.coli beta
                                                                                               sequence of comments)"
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        standard; DNA; 114
                                                                                         /note-
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                     (first
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LT 5
070465 stand
070465;
05-APR-1995
Generic DNA
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                                                          Synthetic
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WPI; 88-279927/40.

Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
Introducing random point mutation of molecules and screening.

Introducing random point mutation of molecules and screening.

Sinclosure; p; English.

Random point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for
reverse transcriptase and the molecules are misincorporated by the
transcriptase and the molecules are misincorporated by the
transcriptase and the molecules are misincorporated by the
cranscriptase and the molecules are substitutions, most of which
occurred singularly in any given mutant.

See also P80575.

See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9418318-A.

D 18-AUG-1994.

D 18-AUG-1994.

F 01-FEB-1993; US-013416.

PR 01-FEB-1993; US-176500.

PR 30-DEC-1993; US-176500.

PR (UYNC-) UNIV NORTH CAROLINA.

PI FOWLKES DM, RAY BK;

DR WPI; 94-279739/34.

PT Identifying proteins or peptide(s) which bind a ligand - by recening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain and an effector domain.

--- Page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7

ID 070469 standard; DNA; 114 BP.

AC 070469;

AC 070469;

DT 07-APR-1995 (first entry)

DE Generic DNA sequence to generate a random TSAR peptide library.

E Generic DNA sequence to generate a random TSAR peptide library.

E Generic DNA sequence to generate a random TSAR peptide library.

EW TSAR; totally synthetic affinity reagent; synthetic; binding domain; KW effector domain; concateneated heterofunctional protein; linker;

EW direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                           elongation
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nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Les
Pred. No. 5.38e-07;
53; Mismatches 35;
                                                   site
                                                                                                                                                                            Koivula A, Bamford J,
                                                 cloning
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6,9 or 12
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55..60
/*tag= a
/note= "this sequence
Location/Qualifiers
19..69
/*tag= a
/function=multiple c
187..204
/*tag= b
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/note= "this
sequence of 6
comments)"
                                                                                                                        30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, K
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h
Similarity 15.1%;
16; Conservative
                                                                                          EP-285123-A.
05-MAY-1988.
30-MAR-1988;
03-APR-1987;
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                  c_feature
                                                               primer_bind
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Best Local S
Matches 1
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CTO0469 is a generic DNA sequence used to generate random TSAR peptide
This generic formula can be represented as follows: X(TGC)(NNB)10-
CTGC)(NNB)6Z(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This
sequence generates peptides that are cloverleaf in structure. Other
concatenated by these generic sequences are shown in R65150-54. TSARs are
generated by these generic sequences are shown in R65150-54. TSARs are
concatenated heterofunctional proteins or peptides, comprising at least
two functional regions - a binding domain with affinity for a ligand and
a second effector peptide portion that is chemically or biologically
active. They may further comprise a linker peptide between the 2 domains.
The oligonucleotides are also designed so that the expressed peptide
contains 2 or 4 cysteine residues. These residues confer some degree of
conformational rigidity to the peptides. The TSARs or comprising
a TSAR binding domain can be used in vivo to deliver a chemically or
biologically active molety, eg. metal ion, radioisotope, peptide, toxin
or enzyme, to the specific target or on the cell. They can also replace
the function of macromolecules, eg. monoclonal or polyclonal antibodies
and therefore circumvent the need for complex methods of hybridoma
characterised and have designed activity allowing direct and rapid
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Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specified by these generic sequences are shown.
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O70468;
O70468;
O5-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
rSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
effector domain; concateneated heterofunctional protein; linker;
afrect; rapid; detection; screening; treatment; generic; ss.
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', 9 or 12 nucleotides
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Sequence 114 BP; 0 A; 4 C
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/note= "this s
sequence of 6
comments)"
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18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 6.3%; 7; Conservative
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4-279739/34.
R65154.
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Best Local
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P-PSDB; R58383.

P-PSDB; R58383.

Identifying proteins or peptide(s) which bind a ligand - by creening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain comprising a binding proteins. Solved to generate random TSAR (Totally CY0472 is a generic DNA sequence this generic formula can also be considered as follows: X(NNB)1(CAC)(NNB)(CAC)(NNB)2Z(NNB)6 considered as follows: X(NNB)1(CAC)(NNB)1(CAC)(NNB)2Z(NNB)6 considered as follows: X(NNB)1(CAC)(NNB)1(CAC)(NNB)2Z(NNB)6 considered as follows: X(NNB)1(CAC)(NNB)1(CAC)(NNB)2Z(NNB)6 considered by this and other generic sequences (Q70470-73) have invariant conscribing and other generic sequences (Q70470-73) have invariant conscribing a long domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active molety, eg. metal control of matternal comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal control cont
R65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker comprise between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      have designed activity
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TSAR; totally synthetic affinity reagent; synthetic; binding domain effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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No. 6.18e-06;
Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34;
Pred. No.
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/note= "encoded by Z
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34;
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01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI; 94-279739/34.
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larity 2.7%;
Conservative
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Q70472 standard; DNA;
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10-APR-1995
Generic DNA
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Terson, Notice and Notice of the period of the processing fusion proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or screening a recombinant vector library expressing fusion proteins or screening a recombinant vector library expressing fusion proteins.

Tomprising a binding domain and an effector domain proteins or page 35: 255pp; English.

Offorciosure; Page 35: 255pp; English.

Synthetic Affinity Reagents) peptides. This generate random TSAR (Totally Cynthetic Affinity Reagents) peptides. This generate formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specified further. Other generated by these general sequences are shown in Q70466-68.

Other specified further. Other generated by these general sequences are shown in Q70466-68.

Comprising at least two functional regions - a binding domain with a fill of the expressed peptide contains 2 or 4 cysteine residues positioned that the expressed peptide contains 2 or 4 cysteine residues positioned to rempse sequences are also designed so confer some degree of conformational rigidity to the peptides. The TSARS or compses. Comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, can also conformations the expressed peptide, tookin or enzyme, to the specific target or on the conformations of the peptide or on the period of the peptide of the peptide of the period of the period of the peptide of the conformation of marrowless or or on the conformation of the peptide of the period of the period of the peptide of t
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monoclonal or polyclonal antibodies and therefore circumvent the for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have design activity allowing direct and rapid detection in a screening profession to 114 BP; 6 A; 12 C; 0 G; 0 T;
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larity 10.7%;
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01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA
FOWIKES DM, KBY BK;
WPI; 94-279739/34.
P-PSDB; R65150 and R65151.
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Tidentifying proteins or peptide(s) which bind a ligand - by
screening a recombinant vector library expressing fusion proteins
occomprising a binding domain and an effector domain
bisclosure; Page 35; 255pp; English.

O70467 is a generic DNA sequence used to generate random TSAR (Totally
Synthetic Affinity Reagents) peptides. This generic formula can also be
conversented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1Y. X
and Y are flanking restriction sites (X is not the same as Y) that are
not specified further. Other generic sequences are shown in Q70466-68.

Other specified further. Other generic sequences are shown in R5515-54. TSARs are concatenated by these generic sequences are shown in
R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
comprising at least two functional regions - a binding domain with
affinity for a ligand and a second effector peptide portion that is
chemically or biologically active. They may further comprise a linker
peptide between the 2 domains. The oligonucleotides are also designed so
that the expressed peptide contains 2 or 4 cysteine residues positioned
in, or flanking, the unpredicted or variant residues. These residues
confer some degree of conformational rigidity to the peptides.
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Complex methods of hybridoma formation of no vivo no the region of the 
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05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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tches 75;
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remaining a binding domain and an effector domain

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bisclosure; Page 35; 255pp; English.

Off0468 is a generic DNA Sequence used to generate random TSAR (Totally Off0468 is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NB)11(TGC)(NNB)5(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q7046-68.

Cother specified further of unctional regions - a binding domain with R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with R65151-54. TSARs are concatenated heterofunctional proteins or peptides for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The Oilgonucleotides are also designed so that the expressed peptide contains 2 or 4 cystelne residues positioned to finat the expressed peptide contains 2 or 4 cystelne residues positioned to finate some degree of conformational rigidity to the peptides. These residues confers some degree of conformational rigidity to the peptides. The readioisotope, peptide, toxin or enzyme, to the specific target or on the readioisotope, peptide, toxin or enzyme, to the specific target or on the conformation or polyclonal antibodies and therefore circumvent the need for conformation function of macromolecules, eg.

Cor compute methods of hybriddoma formation or in vivo antibody placet and rapid detection in a screening process.

Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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070468 standard; DNA; 114 Br.
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05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding don effector domain; concateneated heterofunctional protein; linker; effector domain; concateneated heterofunctional protein; linker; effector apid; detection; screening; treatment; generic; ss.
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recomprising a binding domain and an effector domain
recomprising a generic DNA sequence used to generate random TSAR (Totally
represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)12. X
represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)11. X
represented as follows: X(NNB)16(TGC)(NNB)12(NNB)18
refility for a ligand end e second effector peptide portion that is
comprised at least two functional regions - a binding demain with
compressed peptide contains 2 or 4 cysteine residues
confer some degree of conformational rigidity to the peptides. The TSARs
confer some degree of conformational rigidity to the peptides. The TSARs
confer some degree of conformational rigidity to the specific target or on the
coll. They can also replace the function of macromolecules, eg.
complex methods of hybridoma formation or in vivo antibody production.
The TSARs are easily characterised and have designed activity allowing
direct and rapid detection in a screening process.
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070469;
07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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          domain;
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Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding don effector domain; concateneated heterofunctional protein; linker direct; rapid; detection; screening; treatment; generic; ss.
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US-013416.
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comments)"
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WPI; 94-279739/34.
P-PSDB; R65153.
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WPI; 94-27973
                                                                     direct; rapid
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Key
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01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
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                                                                                                     a TSAR binding domain can be used in vivo to delive, a community, to the specific target or on the cell. They can also replace or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eq. monoclonal or polyclonal antibodies the function of macromolecules, eq. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily formation or in vivo antibody production. The TSARs are easily
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TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                  WO9418318-A.
18-AUG-1994.
01-FEB-1994; 01-FEB-1993; 30-DEC-1993; 31-JAN-1994; 0VNC-) UNIV POWIKES DM,
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Generic DNA S
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PP 18-AGC-1994

PR 01-FEB-1994; U00977.

PR 01-FEB-1993; US-01346.

PR 30-DEC-1993; US-175600.

PR 31-JAN-1994; US-186301.

PA (UTNC-) UNIV NORTH CAROLINA.

PI FOWIKES DW, RAY BK;

DR WIT; 94-2793/34.

PT dentifying proteins or peptide(s) which bind a ligand - by

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

PT STATES DW, RAY BK;

PT GENTIFYING PROTEINS DW SEQUENCE used to generate random TSAR (TOTAILY

PT STATES AFTER SEQUENCE) DWA SEQUENCE USED TO GENERAL SEGUENCES

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Query Match Best Local Similarity 8.2%; Pred. No. 6.81e-05; Matches 9; Conservative 28; Mismatches 73; Indels 0; Gaps

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Db 65 nbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnb 114

GTGGATCTCCTGCTGGTCAGTGGGGGGGGGGGGCAGCACTACCGTGGCCTG

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Search completed: Tue Jul 21 15:26:57 1998 Job time : 113 secs. THIS PAGE BLANK NEWSOND)

09-047-652A-1.rni

US

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. database search, using Smith-Waterman algorithm n.a MPsrch_nn

MasPar time 36.70 Seconds 953.206 Million cell updates/sec Tue Jul 21 15:27:14 1998; Run on:

output not generated. Tabular

>US-09-047-652A-1 (1-652) from US09047652A.seq 652 Title:

...GTTCTTGGAACATGGAATTT CCACGGCGAAGGTCTCCGCT. GGTGCCGCTTCCAGAGGCGA. Ч Description: Perfect Score: N.A. Sequence: Comp:

65

default TABLE Gap 6 table: Scoring

104157 seqs, Searched

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Query

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Dbase

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STD

Nmatch

26825796 bases

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Minimum Match 0% Listing first 45 Post-processing:

summaries

Database:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles

scale 1.696

Variance 4.783;

Mean 8.113;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 22 22 22 22 22 22 22 22 22 22 22 22	81	7	T-0895-	equence 92, Applicat	.97e-0
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11 11 12 13 13 13 13 13 13 13 13 13 13 13 13 13		٦	S-08-47	equence 144, Applica	.10e-0
14 15 16 23 3. 3.		1	-80-S	143, Applica	.10e-0
15 16 17 23 33 3.			S-08-47	equence 142, Applica	.10e-0
16 23 3. 17 23 3.		~	CT-US95-	ce 100, Appl	.10e-0
17 23 3.		~	CT-US95-	ce 99, Applicat	.10e-0
18 23 3		~	CT-US9	ce 98, Applicat	.10e-0
		~	CT-US95-	uence 97, Appli	.10e-0
9 22 3.		-	US-08-471-	5, Applica	.61e-0
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144, Applica 143, Applica 142, Applica 1, Applicati	ce 1, Applicatio ce 1, Applicatio ce 95, Applicati ce 95, Applicati ce 93, Applicati	93, Applicate 2, Application 1, Application 105, Applicat	18, Applicate 85, Applicate 1, Application 49, Applicate 84, Applicate 84, Applicate 84, Applicate 84, Applicate 85, Applicate 8	to 4, Application 25 23, Application 25 120, Application 25, A	ce 25, Applicat ce 9, Applicati
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ALIGNMENTS

Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: BORNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: US/07/935,313 IMMI APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INTELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)883-4109
TELEFAX: (703)683-4109
TELEFX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS: RESULT

ID US-08-232-463-14 S
AC XXXXX
DT SEQUENCE 14, Appli
CC SEQUENCE 14, Appli
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APPLICANT: SCH
APPLICANT: SCH
CC CORRESPONDENCE
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|. No. 1.46e-08;
| Mismatches 98
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One Market
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFOPY
                                                                                                                                                                                                                                                                                                                                                                                                                             S
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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82; M
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Sequence 5, Application US/08238
Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John NAPPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INTITLE OF INVENTION: POLYGAL!
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and TCSTREET: Steuart Street Tov
CITY: San Francisco
STATE: California
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LOCATION: 1..215
OTHER INFORMATION: /stance
OTHER INFORMATION: seques
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Best Local Similarity 13.4%;
Matches 28; Conservative
                                                                                                                          protein
                                                                                                                unknown
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US-08-238-163-5
                                                                                                                TOPOLOGY:
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Tower, One
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COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBER: US/08/238,16
03-MAY-1994
                                                                  1486
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US/08238163
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Pred.
203; M
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INFORMATION:
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GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John
APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT
TITLE OF INVENTION: POLYGA
                                                                  1491
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Steuart Street S
San Francisco
California
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       pairs
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ADDRESSEE: Townsend &
STREET: Steuart Street
CITY: San Francisco
STATE: California
                                                                                    6.0%;
larity 0.3%;
Conservative
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MEDIUM TYPE: Floppy
               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                            IMMEDIATE SOURCE:
CLONE: pT2gpt-F1s
SEQUENCE 7218 BP; 1944 A;
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ATTORNEY/AGENT IN
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US-08-238-163-5
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       LENGTH:
TYPE:
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TOPOLOGY: 11
MOLECULE TYPE:
DUENCE 74 BP; 3
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OLECULE TYPE:
ENCE 81 BP; 3
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ZIP: 10036
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      TELEPHONE:
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CITY: N
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QUENCE 81
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sequence of PGIP from bean.
C; 25 G; 26 T; 141 OTHER.
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Mismatches 95
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NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
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Peptide Libraries
: 103
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Bindin
TITLE OF INVENTION: Peptide Librar
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Pred.
81; M
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
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LOCATION: 1.215
OTHER INFORMATION: /sta
OTHER INFORMATION: sequescible Sequesci
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larity 12.4%;
Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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FILING DATE: 20-SE
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CITY: Ne
STATE: N
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TITLE OF INVENTION: Antigen Binding Peptides (Abtides)
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
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                                                                                                                                                             Length 74;
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1. No. 1.97e-02;
Mismatches 44
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Mismatches
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APPLICATION NUMBER: PCT/US95/1193
FILING DATE: 20-SEP-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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Pred. No.
20; Misma
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Pred. No.
20; Misma
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REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFX: 66141 PENNIE
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(212) 790-9090
12) 869-9741/8864
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C; 6 G; 4
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LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
          TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                               LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1155 Avenue (
New York
New York
                                                                                                                                                           3.8%;
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Best Local Similarity 9.9%;
Matches 7; Conservative
                                                                                                                                                                     Similarity 9.9%, 7; Conservative
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ATTORNEY/AGENT INFO
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INFORMATION FOR SEQ
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Pred. No. 6.50e-02;
20; Mismatches 40;
                                                                                                                               Peptides
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
                                                                           BP
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                                                                                                                     APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Partice OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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PC/TUS951193
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                Sequence 94, Application PC/TUS951193
Sequence 94, Application PC/TUS951193
GENERAL INFORMATION:
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TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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C; 3 G; 1
                                                                           STANDARD; DNA;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 7.7%;
Matches 5; Conservative
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V; 4
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MOLECULE TYPE: DI
UENCE 74 BP; 3 A;
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PCT-US95-11934-94
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GENERAL
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Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides)
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                  (Abtides)
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                  Peptides
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1. No. 6.50e-02;
Mismatches 41
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RR: 1101-196-228
                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILLING DATE: 20-SEP-1995
 Antigen Binding Per
Peptide Libraries
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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                                                                                 Edmonds
of the America
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                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
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Pred.
19; M
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(i)
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LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PCT-US95-11934-99 STANDARD;
APPLICANT: Cytogen Corportitle OF INVENTION: Antititle OF INVENTION: Pept NUMBER OF SEQUENCES: 103 CORRESPONDENCE ADDRESS:
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larity 9.1%;
Conservative
                                                                                 SEE: Pennie & ... 1155 Avenue on New York
                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                    New York
: USA
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SEQUENCE 74 BP; 6 A;
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ATTORNEY/AGENT IN
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                                                                                  ADDRESSEE:
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LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
                                                           18,872
:R: 1101-196-228
     APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding P
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1155 Avenue of the Americas
New York
New York
Y: USA
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Pred. No. (
20; Misma
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PCT-US95-11934-92 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edmonds
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MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
CURRENT APPLICATION DATA
                                                                                                                                                                                                                            Similarity 6.2%;
4; Conservative
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                                                                                                                                                                                 TOPOLOGY: 1
MOLECULE TYPE:
SEQUENCE 75 BP; 1
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CITY: Ne
STATE: N
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ZIP: 100
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Matches
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GENERAL
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Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION: Antigen Binding Peptides (Abtides) Fron TITLE OF INVENTION: Antigen Binding Peptides (Abtides) Fron TITLE OF INVENTION: Peptide Libraries
CORRESPONDENCES: 103
CORRESPONDENCES: 103
CORRESPONDENCE ADDRESS: Abbress: Abbresse: Pennie & Edmonds STREET: 1155 Avenue of the Americas
CITY: New York
COUNTY: USA
ZIP: 10036
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: BM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1101-196-228
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) BEDNESC
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41;
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                                                                                                                                                           e 24; DB 2; L
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Mismatches 40
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Pred. No. 6.50e-
19; Mismatches
                                                                                                    OTHER
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                                                                                                                                                            Score 24;
Pred. No.
20; Misma
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                                                                       (genomic)
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C; 4 G; 5
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 9.1%; 6; Conservative
                                                                                                                                                            3.78;
           single
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STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: DNA (QUENCE 81 BP; 3 A; 5 (
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MOLECULE TYPE:
SEQUENCE 81 BP; 6
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PCT-US95-11934-98
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                                                                                                Peptides (Abtides)
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43;
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|. No. 6.50e-02;
| Mismatches 43
                                                                                                                                                                                                                                     Version
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                                                                                   APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Pept
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                       18,872
SR: 1101-196-228
                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11934

FILING DATE: 20-SEP-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-196-22:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864

TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
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                               82
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Sequence 144, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNC;
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                            PC/TUS9511934
PC/TUS9511934
                                UNC;
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Pred.
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Kay, B. K.
Fowlkes, D. M.
TOTALLY ?
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C; 10 G; 8
                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 82 base pairs
TYPE: nucleic acid
                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                       single
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                            Sequence 97, Application
Sequence 97, Application
GENERAL INFORMATION:
APPLICANT: Cytogen Co
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TOPOLOGY: linear
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US-08-471-052A-144
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SEQUENCE 82 BP; 1
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PCT-US95-11934
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APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 66;
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                                                                                                                                            Version #1.2
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. No. 2.10e-01;
Mismatches 38;
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                                                                                            MEDIUM ...

COMPUTER: IBM PC ....

COMPUTER: Patentin Release #1.0, Vers

SOFTWARE: Patentin Release #1.0, Vers

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,052A

FILING DATE: 06-JUNE-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 1101-179

TELEPHONE: 212 790-9090

TELEPHONE: 212 869-8864/9741

TELEFA: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 144:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
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1N: 530
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US/08471052A
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Pred. No.
18; Misma
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ZIP: 10036-2711
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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DNESS: single
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Sequence 143, Application
Patent No. 5625033
GENERAL INFORMATION:
                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 1155 AV...
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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US-08-471-052A-143
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SEQUENCE 66 BP; 2
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Fowlkes, D. M.
VENTION: Totally Synthetic Affinity Reagents
FORTION: Totally Synthetic Affinity Reagents
                                                                                                                                            Indels
                                                                                                                             Length
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. No. 2.10e-0
Mismatches
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                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    J, ve US/08/471,052A 06-JUNE-1995
                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                    5-2711
DABLE FORM:
JE: Floppy disk
IBM PC compatible
""STEM: PC-DOS/MS-DOS
"Tn Release #1.0, V
       18,872
ER: 1101-179
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US/08471052A
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Pred. No.
18; Misma
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 bases
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DC SOFTWARE: Patentin ReleCURRENT APPLICATION DATA: APPLICATION NUMBER: US, FILING DATE: 06-JUNE-19
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 69 bases
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                                                                                                             S
                                                                            nucleic acid
DEDNESS: single
DGY: unknown
E TYPE: DNA
                                                                                                                                                                                                                                                               Sequence 142, Application U
Sequence 142, Application U
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOWIKES, D.
TITLE OF INVENTION: Tot
                                                                                                                           y Match
Local Similarity 13.4%;
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FOR MEDIUM TYPE: Flor
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US-08-471-052A-142
                                                                                    STRANDEDNESS:
TOPOLOGY: un
MOLECULE TYPE:
SEQUENCE 68 BP; 3
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BP; 2
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                                                                                                                                                                                           61 NNACCTG
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Pred. No. 2.10e-01;
19; Mismatches 42
  DB 1; I
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION: Antigen Binding Partitle OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
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of the Americas
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20-SEP-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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 Score 23;
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17; Misma
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APPLICATION NUMBER: PC
FILING DATE: 20-SEP-19
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Similarity 13.6%;
9; Conservative
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Sequence 100, Application
GENERAL INFORMATION:
APPLICANT: Cytogen Cor
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Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

algorithm Smith-Waterman using search, n.a. database n.a MPsrch_nn

MasPar time 760.50 Seconds 1145.170 Million cell updates/sec 21 15:11:50 1998; Tue Jul Run on:

output not generated.

Tabular

>US-09-047-652A-1 (1-652) from US09047652A.seq 652

.....GTTCTTGGAACATGGAATTT CCACGCCGAAGGTCTCCGCT.. -Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

52

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default TABLE Gap 6 Scoring table:

Query 0 Dbase 0; STD Nmatch

× 667866413 bases seds, 1759237 Searched

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summaries Post-processing:

08 45 Minimum Match Listing first

Database

Database

embl-est54
1:em_est1 2:em_est3
genbank-est106
3:gb_est11 6:gb_est12 7:gb_est13
8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17
12:gb_est18 13:gb_est19 14:gb_est2 15:gb_est20
16:gb_est21 17:gb_est22 18:gb_est3 19:gb_est4 20:gb_est521:gb_est6 22:gb_est7 23:gb_est8 24:gb_est9 25:gb_gss26:gb_sts

Mean 10.452; Variance 2.420; Statistics:

scale 4.319

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

		Eukaryotae; metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 546) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 472.	
RESULT LOCUS DEFINITION	NID KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	FEATURES	source

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Homo sapiens
Eukaryotae; Metazoa; Chordata; Ver
Primates; Catarrhini; Hominidae; H
1 (bases 1 to 572)
NCI-CGAP http://www.ncbi.nlm.nih.g
National Cancer Institute, Cancer
Tumor Gene Index
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Email: Robert_Strausberg@nih.gov Tissue Procurement: L. Jeffrey M
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larity 98.4%;
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/organism="Homo sapiens"
/organism="Homo sapiens"
/note="Organ: larynx; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhOi; Cloned unidirectionally. Primer:
Oligo dT. Larynx. 5' adaptor sequence: 5' GAATTCGGCACGAG
3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'
Average insert size: 0.9 kb."
/db_xref="taxon:9606"
/db_xref="IMAGE:1089215"
/clone_lib="NCI_CGAP_Larl"
/tissue_type="larynx"
/lab_host="SOLR (kanamycin resistant)"
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cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Location/Qualifiers
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larity 96.5%;
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AUTHORS
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        bp mRNA EST 05-FEB-1998
fetal heart NbHH19W Homo sapiens cDNA clone
to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEP11
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                                                                                        Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 567)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 6310
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; consortium (info@image.llnl.gov) for further in:
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 487.
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/lab_host="DH10B (ampicillin resistant)
167 c 175 g 98 t 1 othe
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larity 96.3%;
Conservative
AA775735 567 by zf31f04.s1 Soares for 378559 3' similar to RECEPTOR (HUMAN);, n AA775735 92835069
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AA161033 563 bp mRNA EST 16-DEC-1996
zo58e04.sl Stratagene pancreas (#937208) Homo sapiens cDNA clone
591102 3' similar to gb:U12421_cdsl PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN);, mRNA sequence.
AA161033
g1735356
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

Washu-Merck EST Project
Unpublished (1995)
CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGTGAAGGCCAG
                                                                                                                                                                                                                                                                                                            GCC-AGAGGAAC-ACAGCCTTCTCTGTGAAGCCTCC-AGCTCTTTC-AGAC-AGGTAGGA
                                                                          GGTAGTGTGACTCGCCCCCCCCACTGACCAGCAGGATCCACCAAGGCCCAGCCCATTTG
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                                                                                                                                                                                                                                                     63108
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63101
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; col
IMAGE Consortium (info@image.llnl.gov) for further info
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 425.
Location/Qualifiers
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31 Stratagene pancreas (#937208) Homo sapiens cDNA clone
32 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPI
(HUMAN);, mRNA sequence.
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euthe; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 610)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Washu-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                  CACGGTAGTTGGC-CCGCCGCCCCACTGACCAGCAGGAGATCCACCAAGGCCCAGCCCAT
                                               AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG
                                                                                          CCAGGCCAGGTAAGGGGTAGAGCAGGCGGGGGCCAGCGGGGGCTTCACCTGGTACCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63;
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384
plate of this clone contains both human and mouse des
Thus, the origin of this clone is uncertain. This can
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                         GAGGCCCAGGGGAACCACAGCCTTCTCTGTGAAGCTTCC-AGCTCTTTCCAGA
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1. .610
/organism="Homo sapiens"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-2AP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"
/db_xref="GDB:3917098"
/db_xref="Taxon:9606"
/clone="525669"
/clone="S25669"
/clone="S25669"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
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This clone is available royalty-free through LLNL | IMAGE Consortium (info@image.llnl.gov) for further Insert Length: 951 Std Error: 0.00 Seq primer: -40Ml3 fwd. from Amersham High quality sequence stop: 118.

Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                           /www.ncbi.nlm.nih.gov/ncicgap.
Institute, Cancer Genome Anatomy
                                                                                                                                X.D.,
                                                                                                                                                  Inc.,
                                   tebrata
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Pred. No. 0.00e+00;
0; Mismatches 10;
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                                  Vertebi
                                Eukaryotae; Metazoa; Chordata; Ve
Primates; Catarrhini; Hominidae;
1 (bases 1 to 568)
NCI-CGAP http://www.ncbi.nlm.nih
National Cancer Institute, Cances
                                                                                                       Ph.D
                                                                                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey M
Emmert-Buck, M.D., Ph.D.
                                                                                             Tel: (301) 496-1550
Email: Robert ct.
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Similarity 96.9%;
496; Conservative
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                           Homo sapiens
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/organism="Homo sapiens"
/note="Organ: prostate; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhOI; Cloned unidirectionally. Primer:
Oligo dT. Normal prostate epithelial cell line (HPV
immortalized). 5' adaptor sequence: 5' GAATTCGCCACGAG 3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTT 3'
Average insert size: 1.1 kb."
/db_xref="taxon:9606"
/clone="IMAGE:1175743"
/clone="iMAGE:1175743"
/clone=lib="NCI_CGAP_Pr25"
/tissue_type="epithelium (cell line)"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                           AA643068 591 bp mRNA EST 27-OCT-1997 nr95f04.s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1175743 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
AA643068
92568286
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K.
Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequenc:
clone distribution: NCI-CGAP clone distribution informationd through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammal

Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 591)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy
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High quality sequence stop: 337.
Location/Qualifiers
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Pred. No. C
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Similarity 95.4%;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 428.

Location/Qualifiers

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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euther;
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 541)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project
Unpublished (1997)
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1. No. 0.00e+00;
Mismatches 11;
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/clone="IMAGE:683002"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center/lab_host="DH10B"
complement(<1. .>556)
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 631(
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; cc
IMAGE Consortium (info@image.llnl.gov) for further in:
Insert Length: 598 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 52.
Location/Qualifiers
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1 others
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Pred. No. 0.00e+00
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Similarity 97.9%;
461; Conservative
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18-FEB-1998 IMAGE:1270459

clone

P MRNA EST COB1 HOMO Sapiens CDNA

541 bp NCI_CGAP_G

AA748434 ny01b10.s1

LOCUS

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RESULT

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Center
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  PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
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ب
                                                                                                  Vertebrata; Mammalia;
                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Da
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Seq
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                        Homo sapiens

Eukaryotae; Metazoa; Chordata; Vertebrata; Mammal

Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 541)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy

Tumor Gene Index
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Pred. No. 0.00e+00
0; Mismatches 2:
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Location/Qualifiers
gb:U12421_cds1 mRNA sequence.
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larity 94.7%;
Conservative
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Unpublished (1997)
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similar to
(HUMAN);,
AA748434
g2788392
EST.
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AUTHORS
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/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/db_xref="taxon:9606"
/clone="813186"
/clone="11b="soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     벙
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aa13g10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 813186 3'
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTO!
(HUMAN);, mRNA sequence.
AA456315
g2179525
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
    413
                                 348
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                                                                                                                                                                                                                       527
                                                                                                                                                                                                                                                 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 443.
Location/Qualifiers
1. .506
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                           CCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGCGAAGGCCAG
ACCTGCTGGTGCAGCTGCAGTCCCTGGTGGGCCGGGCACTCTGGCAGCCGCCGTCC
                                                                                                        GTTCGGNAGCAAAGAAGATGGGGGGGCATGAC-ATTTAAGGGCAAGTTGCCCAGTGTAGA
                                                                                          CCAGGCCAGGTAGGGGTAGAGCAGGCGGGCGAGCGGGGCTGCACCTGGTAGCAGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 506)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jo.
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
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k 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashU-Merck EST Project
Washington University School c
4444 Forest Park Parkway, Box
Tel: 314 286 1810
Fax: 314 286 1810
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AUTHORS
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JOURNAL
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KEYWORDS
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COMMENT

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551 bp mRNA EST 10-MAY-1997 s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 'similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE (HUMAN);, mRNA sequence.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 551)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                    AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCGG
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1. No. 0.00e+00;
Mismatches 10;
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available royalty-free
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pregnant uterus"
/lab_host="DH10B"
complement(<1. .>506)
/db_xref="GDB:6044096"
a 150 c 158 g
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WashU-Merck EST Project
Washington University School of
4444 Forest Park Parkway, Box 8:
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty
                                                                                                            Score
Pred.
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IMAGE Consortium (info@image.llnl.gov)
Insert Length: 695 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 321.
Location/Qualifiers
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db_xref="GDB:3758023
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                    .nlm.nih.gov/ncicgap.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Ma
Frimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
Tumor Gene Index
Unpublished (1997)
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Mismatches 21;
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 323.
Location/Qualifiers
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                                                                                                                       Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov Tissue Procurement: Suzanne L. TPh.D.
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CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGCGAAGGCCAG

GTGGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCTCGAC

AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG

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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CONA Library Arrayed by: Greg Lennon, Ph.D.
WWA-bio.libution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/Lint at:
www-bio.linl.gov/bbrp/image/image.html
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Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 543)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
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/lab_host="DH108"
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AA768741 507 bp mRNA EST 08-FEB-1998 ob22g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324464 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR AA768741 g2819456 EST.

Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 507)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
Tumor Gene Index
Unpublished (1997)

human

KEYWORDS SOURCE

ACCESSION NID

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ORGANI

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JOURNAL COMMENT

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                                          Score 394; DB 13;
Pred. No. 0.00e+00;
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/clone="IMAGE:1324464"
/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors
/lab_host="DH10B"
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Unit.K. 3.1A John F. Collins, Biocomputing Research t (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd Release 3. Copyright

algorithm Smith-Waterman using search, database n.a. n.a MPsrch_nn

MasPar time 108.16 Seconds 767.738 Million cell update 21 16:05:14 1998 Tue Jul င္ပ Run

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> not generated output Tabular

>US-09-047-652A-2 (1-652) from US09047652A.seq 652 CCACGGCGAGGGTCTCCGCT ~ Description: Perfect Score: N.A. Sequence: Comp:

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..GTTCTTGGAACATGGAATTT ..CAAGAACCTTGTACCTTAAA

default Scoring table

TABLE Gap 6

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summaries 0.8 4.5 Minimum Match Listing first Post-processing:

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n-geneseg31-2 1:partl 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37

1.561 scale .456; ហ Variance .516; ∞ Mean

. No. is the number of results predicted by chance to have a e greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution. score and is Pred

SUMMARIES

44 6.7 91 9 051746 Oligonucleotide probe 2.41e- 41 6.3 204 1 N81164 Base substituted E.co 1.11e- 40 6.1 91 9 051746 Oligonucleotide probe 3.92e- 40 6.1 91 9 051746 Oligonucleotide probe 3.92e- 36 5.5 114 12 070465 Generic DNA sequence 5.68e- 36 5.2 114 12 070469 Generic DNA sequence 6.48e- 34 5.2 114 12 070469 Generic DNA sequence 6.48e- 34 5.2 114 12 070466 Generic DNA sequence 6.48e- 34 5.2 114 12 070467 Generic DNA sequence 6.48e- 34 5.2 114 12 070467 Generic DNA sequence 6.48e- 34 5.2 114 12 070467 Generic DNA sequence 6.48e- 34 5.2 114 12 070467 Generic DNA sequence 6.48e- 34 5.2 114 12 070467 Generic DNA sequence 6.48e- 34 5.2 114 12 070467 Generic DNA sequence 6.48e- 35 5.1 114 12 070467 Generic DNA sequence 6.48e- 36 5.2 114 12 070467 Generic DNA sequence 6.48e- 37 5.1 114 12 070467 Generic DNA sequence 6.48e-	Ū.	Core	% Query Matich	Length	80	G.	Description	Pred No.
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ALIGNMENTS

WPI; 95-206931/27.

WPI; 95-206931/27.

Identifying gene signatures in 3'-directed human cDNA library - e.g. Identifying gene signatures in 3'-directed human cDNA hat that reflects relative abundance of corresp. mRNA in specific human tissues.

Trissues.

Claim 1; Page 1068; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA which comprises one of the 7837 "Gs" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) concerned by human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) concerned by human genomic DNA was initiated from the corresp various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA in the particular tissue from which it was derived. It constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 272 BP; 43 A; 78 C; 86 G; 51 T; frequency detection; SSULT 1
T22195 standard; cDNA to mRNA; 272 BP.
T22195;
T22195;
Luman gene signature HUMGS03766.
Human gene signature HUMGS03766.
Gene signature; messenger RNA; mRNA; relative abundance; fre human; cloning; mapping; non-biased library; diagnosis; determine sapiens.
Homo sapiens.
W09514772-A1.
O1-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
A (MATS/) MATSUBARA K.
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ID 051746 standard; CDNA; 91 BP.

AC 051746;

DT 31-MAY-1994 (first entry)

DE 011gonucleotide probe MK14-A

KW 011gonucleotide; DNA probe; mycobacteria; disease diagno

KW 011gonucleotide; DNA probe; mycobacteria; disease diagno

KW 55.

Synthetic.

PR 24-MAY-1993; 108325.

PR 26-MAY-1993; 108325.

PR 26-MAY-
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            Length
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            e 238; DB 20; L
l. No. 6.34e-134;
Mismatches 20;
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N81164;
N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase
E.coli beta galactosidase alpha-fragment; Escherichia coli.
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TGGCCGTCACGCTTTCATGACCACTGGGCCTG
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/function=multiple of 187..204
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2; Conservative
            th 36.5% Similarity 92.3% 251; Conservative
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EP-285123-A.

D 05-MAY-1988; 105163.

30-MAR-1988; 105163.

310-MAR-1988; 105163.

310-MAR-1988; 105163.

310-MAR-1988; 105163.

310-MAR-1988; 105163.

310-MAR-1988; 105163.

3110-1987; US-034819.

3110-198-1987; US-034819.

3110-198-1987; US-034819.

3110-198-1987; US-034819.

3110-198-1987; US-034819.

3110-198-1987; US-034819.

3110-198-1987; US-034819.

3110-198-1988; US-03488.

3110-198-1988; US-034888.

3110-198-1988; US-034888.

3110-198-1988; US-034888.

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Claim 3; Page 14; 23pp; English.
Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides
(Q51735). It hybridized to all spp. of mycobacteria
cross reacted to a few non-mycobacterial spp. The pr
be useful as an initial screen for mycobacterial infe
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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35;
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1. No. 1.11e-0
Mismatches
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Pred. No. 3
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Pred. No.
60; Misma
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Q51746 standard; CDNA; 91 BP.
Q51746;
31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; my
ss.
Synthetic.
EP-571911-A.
O1-DEC-1993; 108325.
24-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
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detection and amplification
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8; Conservative
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P-PSDB; R65150 and R65151.

P-PSDB; R65150 and R65151.

Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins comprising a binding domain and an effector domain proteins comprising a binding domain and an effector domain proteins of the screening a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides. Comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with a schemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, es metal ion, calliver a chemically or biologically active moiety, es metal ion, calliver a chemically or biologically active moiety, es metal ion, collines methods of hybridoma formation of macromolecules, es. Conduction of macromolecules, escaped by both or complex methods of hybridoma formation of macromolecules, escaped by bridoma formation of macromolecules.
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                                                                                                Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding dom effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening: trantment.
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N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
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1. No. 5.68e-07;
Mismatches 74;
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5, 9 or 12
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33; M
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US-013416.
US-176500.
US-189331.
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5; Conservative
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SDB; R65150 an
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01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
(UYNC-) UNIV
FOWIKES DM,
O70465 stand
O70465;
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Generic DNA :
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                                                                                                                                                                                                                                                                                                                                                                                Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
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18-AUG-1994.

01-FEB-1994; U00977.

R 01-FEB-1993; US-013416.

R 30-DEC-1993; US-176500.

R 31-JAN-1994; US-189331.

R 0VNC-) UNIV NORTH CAROLINA.

OR WPI; 94-279739/34.

PT Identifying proteins or peptide(s) which bind a ligand - by receening a recombinant vector library expressing fusion promprising a binding domain and an effector domain and an effector domain
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                                                                                                                                                                                                                                                                                                                  n point mutations into nucleic acods - stranded template, annealing a primer, completion of molecules and screening.
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(see
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                                                                                        cloning
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See also P80575.
Sequence 204 BP; 21 A;
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                                                                                                                                                  EP-285123-A.
05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, R
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Q70469 standard; DNA; 114
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by prepn of single strand
misincorporation, complet
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This generic DNA sequence used to generate random TSAR peptide
This generic formula can be represented as follows: X(TGC)(NNB)10-
C (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This
sequence generates peptides that are cloverleaf in structure. Other
c generic sequences are shown in Q70465-68. Other specific peptides
c generated by these generic sequences are shown in R65150-54. TSARS are
concatenated heterofunctional proteins or peptides, comprising at least
two functional regions - a binding domain with affinity for a ligand and
a second effector peptide portion that is chemically or biologically
c active. They may further comprise a linker peptide between the 2 domains.
The oligonucleotides are also designed so that the expressed peptide
contains 2 or 4 cysteine residues positioned in, or flanking, the
unpredicted or variant residues positioned in, or flanking, the
unpredicted or variant residues. These residues confer some degree of
conformational rigidity to the peptides. The TSARS or compsns. comprising
a TSAR binding domain can be used in vivo to deliver a chemically or
biologically active molety, eg. metal ion, radiolsotope, peptide, toxin
or enzyme, to the specific target or on the cell. They can also replace
the function of macromolecules, eg. monoclonal or polyclonal antibodies

The function of macromolecules, eg. monoclonal or polyclonal antibodies
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                                                                                                                                                                                                                                                                                            the function of macromolecules, eg. metal ion, radioisotope, peptide, toxin and therefore circumvent the need for complex methods of hybridoma characterised and have designed activity allowing direct and rapid sequence 114 BP; 0 A; " " "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specific peptides generated by these generic sequences are shown:
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070468;
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
effector domain; concatenening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 114;
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, 9 or 12 nucleotides
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Mismatches 73;
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Pred. No. 31; Mismat
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Similarity 6.3%;
7; Conservative
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Q70468 standard; DNA;
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PI; 94-279739/34.
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01-FEB-1994;
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T dentifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptide(s) which bind a ligand - by
Is cromprising a binding domain and an effector domain
Disclosure; Page 36; 255pp; English.

O70472 is a generic DNA sequence used to generate random TSAR (Totally
C70472 is a generic DNA sequence used to generate random TSAR (Totally
C70472 is a generic DNA sequence used to generate random TSAR (Totally
C70472 is a generic DNA sequence used to generate formula can also be
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C70767(NNB)5(CAC)2(NNB)4. X and Y are flanking restriction sites
C70767(NNB)5(CAC)2(NNB)6. X and Y are flanking restriction sites
C70767(NNB)5(CAC)2(NNB)6. X and Y are flanking restriction sites
C70767(NNB)6(CAC)2(NNB)6. X and Y are flanking restriction sites
C70767(NNB)6(CAC)2(NNB)6. X and Y are flanking domain sequences. TSARs are
C70767(NNB)6(CAC)2(NNB)6. X and Y bettion to be used in the TSARs or comprise a linker peptide between the 2 domains.
C70767(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6(CAC)6(NNB)6
               comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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ity reagent; synthetic; binding domain;
heterofunctional protein; linker;
eening; treatment; generic; ss.
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  concatenated heterofunctional
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Pred. No. 6.48e-06;
34; Mismatches 75;
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18-AUG-1994.

01-FEB-1993; US-013416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.

(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 2.7%; 3; Conservative
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DB; R58383.
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**R P-PSDB; ND315U and ND3121.**

**Indentifying proteins or peptide(s) which bind a ligand - by

**Indentifying proteins or peptide(s) which bind a ligand - by

**Indentifying proteins to peptide(s) which bind a ligand - by

**Indentifying a binding domain and an effector domain

**Disclosure; Page 35; 255pp; English.**

**Comprising a binding domain and an effector domain

**Disclosure; Page 35; 255pp; English.**

**Comprising a binding domain and an effector domain

**Comprising restriction sites (% 1s not the same as 1) that are

**Comprising at least two functions at eshown in (% 10466-68).**

**Comprising at least two functions are shown in (% 10466-68).**

**Comprising at least two functions are also designed so themically or biologically active. They may further comprise a linker affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonuclectides are also designed so that the expressed peptide conformational rigidity to the peptides. The TSARs

**Confer some degree of conformational rigidity to the peptides. The TSARs

**Confer some degree of conformational rigidity to the peptides. The TSARs

**Confer some degree of conformational rigidity to the specific target or on the radioisotope, peptide, toxin or enzyme, to the specific target or on the radioisotope, peptide, toxin or enzyme, to the specific target or on the monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody

**Confer methods of hybridoma formation and antibody and the specific target or an also replace the function of macromolecules, and also replace and therefore circumvent the need or complex methods of hybridoma formation and and antibodies and therefore discussions are also designed and antibodies are also designed and and antibodies are also 
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O70465;
O50465;
O5-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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18-AUG-1994.
01-FEB-1994; U0097.
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30-DEC-1993; US-17.
31-JAN-1994; US-17.
31-JAN-1994; US-18.
(UYNC-) UNIV NORTH FOWIKES DM, KBY BI WPI; 94-279739/34.
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Tidentifying proteins or peptide(s) which bind a ligand - by
Tidentifying proteins or peptide(s) which bind a ligand - by
Tidentifying proteins or peptide(s) which bind a ligand - by
Tidentifying proteins or peptide(s) Tidentifying proteins
Tidentifying a binding domain and an effector domain
Tidentifying a binding domain and an effector domain
Tidentifying a generic DNA sequence used to generate random TSAR (Totally
Synthetic Affinity Reagents) peptides. This generic formula can also be
Tidentifying restriction sites (X is not the same as Y) that are
Totally a generic Other generic sequences are shown in Q70466-68.
The specified further. Other generic sequences are shown in Q70466-68.
The specified further. Other generic sequences are shown in Q70466-68.
The specified further of unctional regions - a binding domain with
Tidentify for a ligand and a second effector peptide portion that is
That the expressed peptide contains 2 or 4 cysteine residues positioned
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That the expressed peptide contains 2 or 4 cysteine residues positioned
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That the expressed peptide contains 2 or 4 cysteine residues positioned
That the expressed peptide, toxin or enzyme, to the peptides. The TSARS
To compsns. Comprising a TSAR binding domain can be used in vivo to
Tadioisotope, peptide, toxin or enzyme, to the specific target or on the
Takes are easily characterised and therefore circumvent the need for
The TSARS are easily characterised and therefore circumvent the need for complex methods of hybridoma formation of macromolecules, eg.
Theore and rank a service and a service and the services and the service and the services and the service and servi
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                                                                                                                                                                                                                                                or 11 Q70467 standard; DNA; 114 BP. Q70467; Standard; DNA; 114 BP. Q70467; 05-APR-1995 (first entry) Generate a random TSAR petide library. Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding dor TSAR; totally synthetic affinity reagent; synthetic; binding dor effector domain; concateneated heterofunctional protein; linker; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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Identifying proteins or peptide(s) which bind a ligand - by accombinant vector library expressing fusion proteins comprising a binding domain and an effector domain comprishing a binding domain and an effector domain can also be specified the proteins of peptides. This generic formula can also be represented as follows: X(NNB) 11,7CC/(NNB) 52(NNB) 7(TCC)(NNB) 10.

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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or screening a recombinant vector library expressing fusion proteins.

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TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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.....GITCTIGGAACAIGGAAITI CCACGGCGAGGGTCTCCGCT.. >US-09-047-652A-2 (1-652) from US09047652A.seq 652 Н Description: Perfect Score: N.A. Sequence: Comp:

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scale 1.692 Variance 4.794; Mean 8.110; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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Sequence 14, Application US/08232463
Septencar: Schools
APPLICANT: DORNER, F. APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCES: 52
CORRESPONDENCES: 52
CORRESPONDENCES: 52
COUNTRY: USA
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: US/07/935,313 DMMI REFERENCE/DOCKET NUMBER: 39,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149 APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768 

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Mismatches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LABAVITCH, John M.
APPLICANT: LABAVITCH, John M.
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF F
TITLE OF INVENTION: POLYGALACTURONASES AN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourts
STREET: Steuart Street Tower, One Marke
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No.
82; Misma
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1.215
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larity 13.4%;
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FILING DATE: 03-MAY
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMAY
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Sequence 5, Application U
Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, A
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,16
                                                           C; 1486
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Sequence 5, Application US/0823816
Patent No. 5569830
GENERAL INFORMATION:
                                                                                Score
Pred.
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03-MAY-1994
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F: Steuart Street
San Francisco
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LABAVITCH, Je
POWELL, Ann
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0.3%;
LENGTH: 7218 base pa
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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                                                                                                   Conservative
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                                                 IE: PTZ9pt-F1s 7218 BP; 1944
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CLASSIFICATION:
ATTORNEY/AGENT IN
                                       SOURCE
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Local Similarity
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STREET: St
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US-08-238-163-5
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APPLICANT:
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STATE:
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TITLE
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Similarity 7; Conser
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MOLECULE TYPE:
SEQUENCE 74 BP; 3
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SEQUENCE 81 BP; 3
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PCT-US95-11934-92
                                                                 STRANDEDNESS
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STREET: 11
CITY: New
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TYPE: n
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Mismatches 95
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R: 1101-196-228
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                n Corporation
: Antigen Binding Pe
: Peptide Libraries
S: 103
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Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding
TITLE OF INVENTION: Peptide Librarie
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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20-SEP-1995
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Pred.
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /sta
OTHER INFORMATION: seque
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larity 12.4%;
Conservative
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ew York
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RY: USA
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est Local Similarity
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PCT-US95-11934-94
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CITY: N
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11934

FILING DATE: 20-SEP-1995
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Pred. No. 2.03e-02;
20; Mismatches 44;
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. No. 2.03e-C
Mismatches
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GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Pe
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-2;
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
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of the Americas
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Pred. No.
20; Misma
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TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEO TO SEQUENCE
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LENGTH: 81 base pairs
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Pennie & 1
1155 Avenue c
New York
New York
Y: USA
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IDNESS: single
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GGCCAGCCAGGCCAGGTAGGGGTAGAGCAGGCGGCGGGCCAGCGGGCTCACCTGGTACCA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                            Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                e.24; DB 2; L
l. No. 6.68e-02;
Mismatches 40
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. Leslie
ER: 18,872
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                                                                                                                                 APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Portite OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103
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Pred. No. (
20; Misma
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                                                                                                          Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
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                                                                                   UNC;
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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C; 3 G; 1
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                                                                                                                                                                                                                                                                                                                                                                                      74 base pairs
ucleic acid
NESS: single
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                   STANDARD;
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7.78;
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Best Local Similarity
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PCT-US95-11934-94
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MOLECULE TYPE:
SEQUENCE 74 BP; 3
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                       Version #1.30
                  Antigen Binding Peptides
Peptide Libraries
103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e 24; DB 2; L
l. No. 6.68e-02;
Mismatches 41
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T; 60 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Pep1
TITLE OF INVENTION: Peptide Libraries
TITLE OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the Americas
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Pred.
19; M
     Corporation
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                                                                                                                                                                              Floppy disk
APPLICANT: Cytogen Corpc
TITLE OF INVENTION: Anti
TITLE OF INVENTION: Pept
NUMBER OF SEQUENCES: 10:
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue c
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.78;
9.18;
                                                                          SEE: Pennie & |
|: 1155 Avenue |
|New York
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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MOLECULE TYPE:
OUENCE 74 BP; 6
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PCT-US95-11934-99
                                                                                                                              COUNTRY: US
ZIP: 10036
                                                                            ADDRESSEE:
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OPERATING
SOFTWARE:
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CITY: N
STATE:
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juence 92, Application PC/TUS9511934
sNERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 2; | Pred. No. 6.68e-02, 20; Mismatches 4
                    FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: single
                                                                                                                                                                                                                                                                                                                                                       OTHER
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sR: 1101-196-228
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   LION DATA:
MBER: PCT/US95/11934
20-SEP-1995
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APPLICATION NUMBER: PCT/US95/1193
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       61
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
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ADDRESS:
-: Pennie & Edm.
-: 1155 Avenue of t
New York
Y: USA
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 6.2% 4; Conservative
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CURRENT APPLICATION D
APPLICATION NUMBER:
FILING DATE: 20-SE
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MOLECULE TYPE:
OUENCE 75 BP; 1
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PCT-US95-11934-92
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STREET: 11
CITY: New
STATE: New
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OPERATING
SOFTWARE:
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Best Local S
Matches
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Sequence
GENERAL
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                                                                    Length 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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                                                                    e 24; DB 2; L
. No. 6.68e-02;
Mismatches 40
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1. No. 6.68e-02;
Mismatches 41
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                                         OTHER
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Pep
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
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Pred. No.
19; Misma
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PC/TUS9511934
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APPLICATION
FILING DATE: 20-SL
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
LENGTH: 81 base pairs
TWPE: nucleic acid
                                                                                                                                                                                                                                                                    STANDARD; DNA; UNC;
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E: Floppy disk
IBM PC compatible
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Pred.
20; M
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C; 4 G; 5
                           (genomic)
C; 6 G; 4
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Best Local Similarity 9.1%;
Matches 6; Conservative
STRANDEDNESS: single TOPOLOGY: linear
                                                                  Similarity 7.7%;
5; Conservative
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Sequence 98, Application
GENERAL INFORMATION:
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OPERATING SYSTEM:
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RY: USA
10036
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           TOPOLOGY: line
MOLECULE TYPE: D
SEQUENCE 81 BP; 3 A;
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PCT-US95-11934-98
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MOLECULE TYPE:
SEQUENCE 81 BP; 6
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STATE: N
COUNTRY:
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                                                                 Query Match
Best Local
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                                                              APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                e 24; DB 2; Len I. No. 6.68e-02; Mismatches 43;
                                                                                                                                                                                                                Version
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         ВP
                                                                                                                                                                               COMPUTER: IBM r.
COMPUTER: IBM r.
COMPUTER: Batentin Release #1.0, v...
SOFTWARE: Patentin Release #1.0, v...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-27
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                           STALL
COUNTRY: U...
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMEDIUM TYPE: Floppy disk
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Pred. No. (
19; Mismat
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US/08471052A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; UNC;
         UNC;
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                                   PC/TUS95119
PC/TUS95119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 144, Application US/08471
Sequence 144, Application US/08471
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOWIKES, D. M.
TITLE OF INVENTION: Totally S)
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
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         DNA;
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         STANDARD;
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Best Local Similarity 10.1%;
Matches 7; Conservative
                                 Sequence 97, Application
Sequence 97, Application
GENERAL INFORMATION:
APPLICANT: Cytogen Co
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MOLECULE TYPE:
QUENCE 82 BP; 1
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US-08-471-052A-144
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No. 2.15e-01;
Mismatches 38;
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                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-179
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEFAX: 212 869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
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US-08-471-052A-143 STANDARD; DNA; UNC; 68
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of the Americas
 the Americas
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Sequence 143, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Syntheticand NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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larity 9.7%;
Conservative
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STREET: 1155 Avenue C
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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TOPOLOGY: un
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STREET:
CITY: Ne
STATE: N
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Mismatches 40;
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N: 530
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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Pred. No.
18; Misma
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US/08471052A
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3R: 1101-
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                        Edmonds of the 1
                                                                                                                                                                                                                                                                                                   Sequence 142, Application US/0847.
Sequence 142, Application US/0847.
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOWIKES, D. M.
TITLE OF INVENTION: Totally S.
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 69 bases
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Local Similarity 13.4%;
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SOFTWARE: Patent
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CLASSIFICATION:
ATTORNEY/AGENT IN
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US-08-471-052A-142
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TOPOLOGY: u
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UENCE 69 BP; 2
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STREET: 11
CITY: New
STATE: New
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                        40;
 e 23; DB 1; L
1. No. 2.15e-01;
Mismatches 40
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Pred. No. 2.15e-01
19; Mismatches 4
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                               ВР
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                                                                                                                                                                             74
                                                                                                                                                                                                                                                   APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Pa
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  SSEE: Pennie & Edmonds
T: 1155 Avenue of the America
New York
: New York
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                 Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

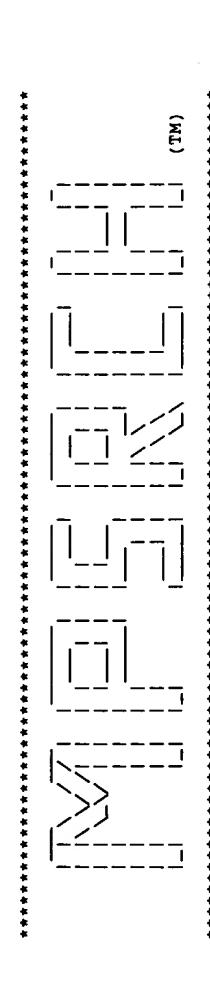
SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
Score 23;
Pred. No.
17; Misma
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larity 9.0%;
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Conservative
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MOLECULE TYPE:
SEQUENCE 74 BP; 6
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STREET: 11
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STATE:
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Query Match
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Matches
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ch Unit. U.K. Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd

Smith-Waterman algorithm using search, database n.a. n. a MPsrch_nn

MasPar time 760.56 Seconds 1145.078 Million cell updates/sec 1998; 21 15:51:59 Jul Tue : 00 Run

not generated output Tabular

>US-09-047-652A-2 (1-652) from US09047652A.seq 652

..GTTCTTGGAACATGGAATTT ..CAAGAACCTTGTACCTTAAA CCACGGCGAGGGTCTCCGCT Н Description: Perfect Score: N.A. Sequence: Comp:

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default TABLE Gap 6 Scoring table:

Query ô Dbase STD Nmatch

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~ × 667866413 bases seds, 1759237 Searched

Post-processing:

summaries 0 4 5 5 Match first Minimum Listing

Database:

Database

embl-est54
1:em_est1 2:em_est3
genbank-est106
3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13 8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17 12:gb_est18 13:gb_est19 14:gb_est2 15:gb_est20 16:gb_est21 17:gb_est22 18:gb_est3 19:gb_est4 20:gb_21:gb_est6 22:gb_est7 23:gb_est8 24:gb_est9 25:gb_gs:26:gb_sts

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scale 4.313 Variance 2.423; 10.451; Mean Statistics

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No. score grea and is der

# SUMMARIES

Pred. No.	.00e	0.00e+00	0.00e+00	.00e+	.00e+	.00e+	.00e+	0.00e+00	.00e+	.00e+	.00e+	0.00e+00	•
	Soares NFL	NCI_CGAP_La	Soares feta	rata	tratag	I_CGAP_	CGAP	CGAP_	Soares ovar	NCI_CGAP_GC	Soares NhHM	H	NCI_CGAP_Pr
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726408-728711, and 729096-731399.
Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="1327269"
/clone_lib="Soares NFL T GBC S1"
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Tel: (301) 496-1550
Email: Robert_Strausberg@n:
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     cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 487.
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1 (bases 1 to 567)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Josi Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project
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Washington University School o
4444 Forest Park Parkway, Box
Tel: 314 286 1800
Fax: 314 286 1810
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euthe; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 610)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
WashU-Merck EST Project
Unpublished (1995)
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 38
plate of this clone contains both human and mouse de
Thus, the origin of this clone is uncertain. This ca
kept in mind should you use this clone.
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Similarity 96.2%;
513; Conservative
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/organism="Homo sapiens"

/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhOI; Cloned unidirectionally. Primer:
Oligo dT. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"
/db_xref="GDB:3917098"
/db_xref="taxon:9606"
/clone="525669"
/clone="525669"
/clone="525669"
/clone="525669"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
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This clone is available royalty-free through IMAGE Consortium (info@image.llnl.gov) for furnert Length: 951 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 118.
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/organism="Homo sapiens"
/note="Organ: lung; Vector: Bluescript SK-; Site_1: EcoRI;
Site_2: xhoI; Cloned unidirectionally. Primer: Oligo dT.
Bulk lung tumor. 5' adaptor sequence: 5' GAATTCGCACGAG 3'
3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT
Average insert size: 1.1 kb."
/db_xref="taxon:9606"
/db_xref="IMAGE:979910"
/clone="IMAGE:979910"
/clone=lib="NCI_CGAP_Lu1"
/tissue_type="lung tumor"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                   Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mamma Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 568)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Tumor Gene Index
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 265.
Location/Qualifiers
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Pred. No. 0.00e+00
0; Mismatches 10
                                                                                                                                                                                                 cDNA Library Preparation: Stratagene, Ph.D. cDNA Library Arraving.
                                                                                                                                             Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov Tissue Procurement: L. Jeffrey M. Emmert-Buck, M.D., Ph.D.
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96.9%;
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/organism="Homo sapiens"
/note="Organ: prostate; Vector: Bluescript SK-; Site_1:
EcoRi; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Normal prostate epithelial cell line (HPV
immortalized). 5' adaptor sequence: 5' GAATTCGCCACGAG 3'
3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'
Average insert size: 1.1 kb."
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/clone_lib="NCI_CGAP_Pr25"
/clone_lib="NCI_CGAP_Pr25"
/tissue_type="epithelium (cell line)"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                           AA643068 591 bp mRNA EST 27-OCT-1997 nr95f04.s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1175743 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR AA643068 g2568286 EST.
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mamma]
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 591)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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High quality sequence stop: 337.
Location/Qualifiers
1. .591
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Email: Robert_Strausberg@nlh.gov Tissue Procurement: Suzanne L. Teph.D.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 428.

Location/Qualifiers

1. .556
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National Cancer Institute, Cancer Oumor Gene Index
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euther: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 541)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Josi Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project
Unpublished (1997)
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/db_xref="taxon:9606"
/clone="IMAGE:683002"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center
/lab_host="DH10B"
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;
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 631
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; consortium (info@image.llnl.gov) for further infoment Length: 598 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 52.
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AA748434 541 bp mRNA EST 18-FEB-1998 ny01b10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270459

AA748434

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                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                               Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mamma]
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 541)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 358.
Location/Qualifiers
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Pred. No. 0.00e+00
0; Mismatches 2:
                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento
Bonaldo, Ph.D.
                                                                                                                                                                                                          Ph.D
                                                                                                                                                                                     Tel: (301) 496-1550
o gb:U12421_cds1
mRNA sequence.
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larity 94.7%;
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WashG-Merck EST Project
WashG-Merck EST Project
Washigton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@waston.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 443.

Location/Qualifiers

1. .506
/organism="Homo sapiens"
/note="Toganism="Homo sapiens"
/note="Toganism="Toganism="Homo sapiens"
/no
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| Soares NhHMPu S1 Homo sapiens cDNA clone 813186 3'
| gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
| mRNA sequence.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominida
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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jo
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
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zk30b07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone
472021 3' similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN);, mRNA sequence.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,l
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)
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/db_xref="GDB:6044096"
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WashU-Merck EST Project
Washington University School of
4444 Forest Park Parkway, Box 8:
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty
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Similarity 96.9%;
463; Conservative
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                                                                                          double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library vent through one round of normalization. Library constructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="472021"
/clone="11b="Soares pregnant uterus NbHPU"
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                              .nlm.nih.gov/ncicgap.
e, Cancer Genome Anatomy
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       Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 505)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncice
National Cancer Institute, Cancer Genome I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 405; DB 16;
Pred. No. 0.00e+00;
0; Mismatches 21;
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 323.
Location/Qualifiers
1. .505
                                                                                                                                                Topalian,
                                                                                               Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Suzanne L. To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.1%;
larity 94.9%;
Conservative
                                                                                  Unpublished (1997)
Homo sapiens
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DNA
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Information can be
                                                                                                                      AA805072 543 bp mRNA EST 19-FEB-1998 ob86c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338240 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOF AA805072 g2873972 EST.
                                                                                                                                                                                                                                                                                Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 543)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
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457
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               GGTAGTGGCTGCCGCCCCCACTGACCAGCAGGAGTCCACCAAGGCCCAGCCCATTTG
 GGTAGTIGICCCGCCCCCCCACTGAC - AGCAGGAGATCCACCAAGGCCCAGCCCATTGG
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                             TCGGGCACCAAAGAAGGATGGGGGGCATGGCAAGTTCAGGGGCAGCTG
                                                                             TCGGGCACCAAAGAAGATGGGGGGCCATGCCCAGTTCAGGGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Ph.D., Gerald Marti, M.D.
cDNA_Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 903 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 272.
Location/Qualifiers
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Pred. No. 0.00e+00
0; Mismatches 23
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AAATICCAIGITCCAAGAACAIGCTCTAAGCAIGCAGAAAGCACAGGACACIGCTCCCGG

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AA768741 507 bp mRNA EST 08-FEB-1998 ob22g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324464 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
AA768741
92819456
EST.
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                           Score 394; DB 13;
Pred. No. 0.00e+00
0; Mismatches 1:
/clone="IMAGE:1324464"
/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors
/lab_host="DH10B"
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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U.
Distribution rights by Oxford Molecular Ltd

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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

scale 0.220 Variance 140.986; Mean 31.057; Statistics

chance to have a result being printed score distribution. predicted by score of the No. is the number of results predigreater than or equal to the score derived by analysis of the total and is Pred.

### SUMMARIES

Pred. No.	189		.89e+	.89	.89	.89e+	.89e+	.89e+	.89e+	.89e+	.89	.89	. 89	φ.	.89	.89	ω.	.89	. 89
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## ALIGNMENTS

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W09623873-A1.

W08-AUG-1996.

WR 29-EBB-1995; DK-000126.

WR 29-EBB-1995; DK-000126.

WR 29-SEP-1995; DK-001037.

WR 29-SEP-1995; DK-001121.

WR 29-SEP-1995; DK-001121.
W12136 standard; protein; 483 AA.
W12136;
W12136;
08-APR-1997 (first entry)
Alpha-amylase variant L351C+M430C+Y243F+delta183+delta184+Q391E+K444Q.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
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PR 09-FEB-1995; DK-000126.

PR 19-FEB-1995; DK-000126.

PR 29-WAR-1995; DK-000126.

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activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and beer-making processes. These variants can also be used in the production of sweeteners and ethanol from starch.
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08-APR-1997 (first entry)
Alpha-amylase variant delta182 + delta184.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme
Alpha-amylase; detergent; thermal stability; vashing composition;
calcium ion dependency; alpha-amylolytic activity; washing composition;
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Pred. No. 5.89e+
8; Mismatches
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Pred. No. 5.89e+
8; Mismatches
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les 14; Conservative
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standard; protein;

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RESULT

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W12138 standard; protein; 483 AA.
W12138;
W12138;
W12138;
08-APR-1997 (first entry)
Alpha-amylase variant delta181 + delta183.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme; Alpha-amylase; detergent; thermal stability; washing composition; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                   enzyme;
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08-APR-1997 (first entry)
Alpha-amylase variant delta183 + delta184.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzymalpha-amylolytic activity; washing composition; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
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Mismatches
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e created
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Pred. No. 5
8; Mismat
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Synthetic.
WO9623873-A1.
08-AUG-1996.
05-FEB-1995; DK-000126.
29-MAR-1995; DK-001097.
06-OCT-1995; DK-001121.
(NOVO ) NOVO-NORDISK AS.
Bisgard-frantzen H, Borchert T, WPI; 96-371423/37.
Alpha-amylase variants - with impstability and reduced calcium ior Example 2; 111pp; English.
W12098-W12144 represent alpha-amyvariants of the invention were constants of the invention were constants.
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14; Conservative
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Matches
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The Will99 standard; protein; 483 AA.

Will9139 standard; protein; 483 AA.

Will9239; Mill of Garder, thermal stability; oxidation stability; enzyme;
Alpha-amylase variant deital81 + deital82.

Will of Alpha-amylase variants of the modernection; sweetener.

Synthetic.

mutagenesis of the DNA sequences encoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12137-W12140, and C w12143 are specifically variants of the alkaphilic Bacillus strain NCIB 12513 alpha-amylase shown in R81836. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees C celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and beer making processes. These variants can also be used in the production
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10;
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I. No. 5.89e+00;
Mismatches 10
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Pred. No. 5.89e+
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
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Pred. No. 5
8; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                              The alpha-amylase variants beer-making processes. These variants of sweeteners and ethanol from starch.
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14; Conservative
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14; Conservative
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12139 stand
12139;
8-APR-1997
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W09623873-A1.

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W09623873-A1.

W09623873-A1.

W09623873-A2.

WAR-1995; DK-000136.

B1994246_FEB-1995; DK-000136.

WAR-1995; DK-000136.

WAR-1995; DK-001037.

WOVO NOVO-NORDISK AS.

B1994246_FEB-1995; DK-001121.

WOVO NOVO-NORDISK AS.

Alpha-amylase variants - with improved thermal and oxidation

Alpha-amylase variants - with improved thermal and oxidation

Alpha-amylase variants - with improved thermal and oxidation

T stability and reduced calcium ion dependency

Example 2: 111pp; English.

W12098-W12144 represent alpha-amylase variants of the invention. The

W12098-W12144 represent alpha-amylase sencoding the parent alpha-amylases

C variants of the DNA sequences encoding the parent alpha-amylases

represented by W12955, W12956, R81835 and R81836. W12137-W12140, and

W1213 alpha-amylase shown in R81836. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees

Celcius), and/or oxidation stability, and/or reduced calcium ion

Celcius), and/or oxidation stability, and/or reduced calcium ion

Celcius), and/or oxidation stability, and/or reduced calcium ion

Celcius), and of or oxidation stability, and/or reduced calcium ion

Celcius), and of or oxidation stability, and/or reduced calcium ion

Celcius), and etergent and washing compositions, and for textile desizing.

The alpha-amylase variants can also be used in papermaking and

Celcium of the manylase variants can also be used in the production

Conserved or partiants can also be used in the production

Conserved or cleaved or cleaved or second or conserved or cleaved or cleav
                                                                                                                                                08-APR-1997 (first entry)
Alpha-amylase variant delta183 + delta184 + M202L/I.
Alpha-amylase, detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coxidation stability; enzyme; civity; washing composition; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 483;
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W12115;
W12115;
08-APR-1997 (first entry)
Alpha-amylase variant delta181 + delta182.
Alpha-amylase; detergent; thermal stability; oxidation stacelcium ion dependency; alpha-amylolytic activity; washing textile desizing; papermaking; beer-making; ethanol productive sweetener.
Synthetic.
W09623873-A1.
08-AUG-1996.
05-FEB-1996; DK-000126.
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5.89e+00;
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Pred. No. 5.89e+
8; Mismatches
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wvlgpvw-gilysamGygsylvwkelggeTekavv
Location/Qualifiers
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14; Conservative
                                                                                                        protein;
                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                             W12140;
08-APR-1997
                                                                                                                                                                                                                                                               sweetener.
Synthetic.
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Best Local S
Matches 1
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W12140
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Gaps

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Indels

10;

75

wi-ppawkgtsqndvgygaydly-dlgefnqkgtv

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**Net; yo-3/1423/3/.
**Alpha-amylase variants - with improved thermal and oxidation
stability and reduced calcium ion dependency
claim 9; illipp; English.
**Variants of the invention were created using site directed, or random,
contagenesis of the DNA sequences encoding the parent alpha-amylases
contagenesis of the DNA sequences encoding the parent alpha-amylases
contagenesis of the DNA sequences encoding the parent alpha-amylases
contagenesis of the DNA sequences encoding the parent alpha-amylases
contagenesis of the DNA sequences encoding the parent alpha-amylase
contagenesis of the DNA sequences encoding the parent alpha-amylase
contagenesis of the DNA sequences of the alkaphilic Bacillus
contagenesis of the DNA sequences of the alkaphilic Bacillus
contagenesis of the DNA sequences of the alpha-amylases also
contagenesis of the DNA sequences of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing.
The alpha-amylase variants can also be used in the production
contagenesis of the DNA sequences can be analyzed to the DNA sequences can be used in papermaking and beer-making processes. These variants can also be used in the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Woofstand ussizing; papermanning; beer making; enhance production;

Synthetic.

Woofstand-1996.

De-Aug-1996; DK00056.

De-FEB-1995; DK-000126.

R 19-FEB-1995; DK-000126.

R 29-SEP-1995; DK-001121.

R NOVO NOVO-NORDISK AS.

Bisgard-frantzen H, Borchert T, Svendsen A;

R NOVO NOVO-NORDISK AS.

Bisgard-frantzen H, Borchert T, Svendsen A;

R NOVO NOVO-NORDISK AS.

Bisgard-frantzen H, Borchert T, Svendsen A;

R 19-5371423/37.

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Alpha-amylase variant delta183 + delta184.
Alpha-amylase, detergent; thermal stability; oxidation stability; enzyme; Alpha-amylase; detergent; thermal stability; washing composition; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00
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Pred. No. 5.89e+00
8; Mismatches 1
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                                                                                     Svendsen
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29-SEP-1995; DK-001097.
06-OCT-1995; DK-001121.
(NOVO ) NOVO-NORDISK AS.
Bisgard-frantzen H, Borchert
WPI; 96-371423/37.
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Best Local Similarity 40.0%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein;
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W12116 stand
W12116;
08-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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WPI: 96-371423/3.

The property of a contents of the improved a stability and reduced calcium ion dependency stability and reduced calcium. The contents of the invention were created using site directed, or random, contragenesis of the DNA sequences encoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141, Contents of the alkaphilic Bacillus contraints of the manual stability variants of the alkaphilic Bacillus within NCIB 12512 alpha-amylase shown in R81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylases also contivity with respect to cleavage of substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can content and processes improved stability compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and hear-making processes. These variants can also be used in the production the making processes. These variants can also be used in the production the content of the starch.
                  production
                                                                                                                                                                                                                                                          08-APR-1997 (first entry)
Alpha-amylase variant L351C + M430C + delta183 + delta184.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
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    in papermaking
lso be used in
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.89e+00;
ches 10;
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                 can also
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5.89e+00;
                                                                                         . No. 5.89e+
Mismatches
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                                                                          Score 100; I
Pred. No. 5.8
8; Mismatch
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WVLGPVW-GTLYSAMGYGSYLVWKELGGFTEKAVV
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sees. These variants
ethanol from starch.
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Pred. No. 5
8; Mismat
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Bisgard-frantzen H, Borchert
WPI; 96-371423/37.
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larity 40.0%;
Conservative
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14; Conservative
The alpha-amyrass. The beer-making processes. The of sweeteners and ethanol source 483 AA;
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DK-000126.
DK-000336.
DK-001097.
DK-001121.
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14; Conser
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08-AUG-1996.
05-FEB-1996;
03-FEB-1995;
29-MAR-1995;
29-SEP-1995;
06-OCT-1995;
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W12134 stand
W12134;
08-APR-1997
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483

standard; protein;

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sweetener.
Synthetic.
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Best Local S
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W09623873-A1.

W08-AUG-1996.

WR 29-KEB-1996 DK0026.

RR 29-MAR-1995; DK-000126.

RR 29-MAR-1995; DK-000136.

RR 29-MAR-1995; DK-000136.

RR 29-MAR-1995; DK-001037.

RR 209-W12144 represent alpha-amylase variants of the invention. The variants of the invention were created using site directed, or random, uniquenced by W12955, W12956, R81835 and R81836. W12098-W12136, W12141.

W12142 and W12144 are specifically variants of the arapentures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion degreed clouds, and/or reduced calcium ion degreed alpha-amylase also have increased alpha-amylolytic activity (especially at pW values in the range of 80-510.5), and improved binding of a particular substrate. These variant alpha-amylolytic activity (especially with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The maylase variants can also be used in the production harm washing processes. These variants can also be used in the production harmon the may and the may an
08-APR-1997 (first entry)
Alpha-amylase variant Ri24P + delta183 + delta184.
Alpha-amylase, detergent; thermal stability; oxidation stability; enzyme Alpha-amylase; detergent; thermal stability; washing composition; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ന
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W31500 standard; protein; 485 AA.

W31500;

W31500;

08-APR-1998 (first entry)

Bacillus sp. alpha amylase.

Alpha amylase; hard surface cleaning; dishwashing; launding Bacillus sp.

12-SEP-1997.

04-MAR-1996; WO-U03276.

(PROC ) PROCTER & GAMBLE CO.

Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS, Ward G;

WPI: 97-457524/42.

Detergent compositions for hard surface cleaning and laur contains Bacillus derived alpha amylase with improved thermostability, reduced calcium ion dependency etc.

Claim 1; Pages 88-89; 97pp; English.

The present sequence is a Bacillus sp. alpha amylase with specific activity at least 25% higher than that of Terman at 25 to 55 degrees C at pH 8 to 10, measured by the Phac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 5.89e+
8; Mismatches
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|: | | | | : : | | | : | | 47 WVLGPVW-GTLYSAMGYGSYLVWKELGGFTEKAVV
                                                                                                                                                                              Location/Qualifiers
124
/label- R124P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 40.0%;
14; Conservative
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Synthetic.
Key
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detergent; thermal stability; oxidation stability; enzyme; ependency; alpha-amylolytic activity; washing composition; ing; papermaking; beer-making; ethanol production;
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as (RTM)
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04-MAR-1997; U03635.

R (PROC ) PROCTER & GAMBLE CO.
I Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S,
Showell MS, Ward G;
WPI; 97-457524/42.

Thermostability, reduced calcium ion dependency etc.
Thermostability, reduced calcium ion dependency etc.
Thermostability, reduced calcium ion dependency etc.
Thermostability at least 25% higher than that of Termamyl (RTM) at least 25% higher than that of Termamyl (RTM) at 25 to 55 degrees C at pH % to 10, measured by the Phadebas (RT activity test. It is of use in hard surface cleaning, hand or machine dishwashing and laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain removal and fabric care are degrees C. Improved cleaning, stain removal and fabric care are
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activity test. It is of use in hard surface cleaning, hand cannot machine dishwashing and laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain removal and fabric care obtained by using it at a concentration of 0.00018 to 0.06%
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                                                                                                        ; DB 27;
5.89e+00;
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Pred. No. 5.89e+00
8; Mismatches 1
                                                                                                        Score 100; DB 2
Pred. No. 5.89e+
8; Mismatches
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alpha amylase.
e; hard surface
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variant E1940
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W12130;
08-APR-1997 (first entry)
Alpha-amylase variant E1940
Alpha-amylase; detergent; t
calcium ion dependency; alp
textile desizing; papermaki
                                                                                                       Similarity 40.0%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 40.0%;
14; Conservative
                                                                                                                                                                                                                                                                                      protein;
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08-AUG-1996.

05-FEB-1996; DK00056.

03-FEB-1995; DK-000126.

29-MAR-1995; DK-001097.

29-SEP-1995; DK-001097.

06-OCT-1995; DK-001121.

(NOVO ) NOVO-NORDISK AS.
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                                                    by using it 485 AA;
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                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                ESULT 12

W31499 standard;

C W31499;

C W31499;

T 08-APR-1998 (fi

E Bacillus sp. alp

W Alpha amylase; h

S Bacillus sp.

N W09732961-A2.

D 12-SEP-1997; U03

R 07-MAR-1996; WO-
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        Apha-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency

Stability and reduced calcium ion dependency

Claim 11; illpp; English.

W12098-W12144 represent alpha-amylase variants of the invention. The variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases

Crepresented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141, W12142 and W12144 are specifically variants of the alkaphilic Bacillus strain NCIB 12512 alpha-amylase shown in R81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion degrees Celcius), and/or oxidation stability, and/or reduced calcium ion degrees Celcius), and/or oxidation stability, and/or improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and beer-making processes. These variants can also be used in the production of servences.
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WO9623873-A1.

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WO9623873-A1.

WO9623873-A1.

WO9623873-A1.

WO9623873-A1.

WO9623873-A1.

WO9623873-A2.

WO96295 DK-000126.

WOSPEN-1995; DK-000126.

WOSPEN-1995; DK-001037.

WOO-NORDISK AS.

Bisgard-frantzen H, Borchert T, Svendsen A;

WOVO'N WOVO-NORDISK AS.

Bisgard-frantzen H, Borchert T, Svendsen A;

WOSPEN-1995; DK-001121.

WOSPEN-1995; DK-001121.

WOO-NORDISK AS.

Bisgard-frantzen H, Borchert T, Svendsen A;

WOO-NORDISK AS.

Bisgard-frantzen H, Borchert T, Svendsen A;

WOO-NORDISK AS.

WOO-NOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14

ID W12131 standard; protein; 485 AA.

AC W12131;

DT 08-APR-1997 (first entry)

DE Alpha-amylase variant N106D.

KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;

KW Alpha-amylase; detergent; thermal stability; washing composition;

KW calcium ion dependency; alpha-amylolytic activity; washing composition;

KW textile desizing; papermaking; beer-making; ethanol production;
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by of Termamyl
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This alpha-amylase protein is characterized by having a specific activity at least 25% higher than the specific activity of Termamy at 125-55 deg C and a pH of 8-10. The enzyme can be used in detergent composition for starch liquefaction, the production of lignocellulosic materials, e.g. pulp, paper and cardboard from was containing starch, for deinking recycled starch-coated, or starch-containing printed paper, to modify starch for papermaking, for textile desizing, and beer-making processes. This protein may be produced recombinantly.
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alkaline alpha-amylase.
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The alpha-amylase variants beer-making processes. The of sweeteners and ethanol Sequence 485 AA;
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DE Bacillus sp. alkaline al
KW Alpha-amylase; enzyme; E
KW beer; starch.
OS Bacillus.
PN W09526397-A1.
PD 05-OCT-1995; DK0142.
PR 29-MAR-1995; DK-000353.
PR 03-NOV-1994; DK-0001271.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

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Tabular output not generated.

Title: Description: Perfect Score: Sequence:

РАМ 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

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scale 0.405 Mean 41.783; Variance 103.237; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Garnier, M.; Dimchev, A.b.; Douglas, ...,
N.A.; Papadopoulos, V.
Mol. Pharmacol. (1994) 45:201-211
In vitro reconstitution of a functional peripheral-
benzodiazepine receptor from mouse Leydig tumor of a MUID:94158796
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M.R.; Grayson, D.R.; Guidotti, A.; Krueger,
J. Biol. Chem. (1989) 264:20415-20421
Molecular cloning and expression of cDNA encoc
peripheral-type benzodiazepine receptor.
                                                                                 from GB/EMBL/DDBJ
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##cross-references GB:J05122; NID:g206161; PID:g206162
This protein is located mainly in the mitochondrial
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benzodiazepine receptor, mitochondrial - rat
peripheral-type benzodiazepine receptor PKBS
#formal_name Rattus norvegicus #common_name Na0-Sep-1993 #sequence_revision 30-Sep-1993 #t
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Grayson, D.R.; Krueger, K
Gene (1992) 121:377-382
Structure of the rat gene e
benzodiazepine receptor.
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Induction of peripheral-type benzodiazepine receptors during
differentiation of mouse erythroleukemia cells. A possible
involvement of these receptors in heme biosynthesis.
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Ithors Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, I Gene (1995) 155:201-205
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The human peripheral benzodiazepine receptor gene: and characterization of alternative splicing in tissues and in a patient with congenital lipoid
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Regan, J.W.; Laird II, H.E.
Biol. Chem. (1991) 266:14082-14087
Coning and expression of a pharmacologically
peripheral-type benzodiazepine receptor isoc
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                                                                                                                                                                                                                                                                S04404 #type complete
crtK protein - Rhodobacter capsulatus
#formal_name Rhodobacter capsulatus
28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
09-Sep-1997
S04404
SNCE
S04401
Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.E.
hournal
Mol. Gen. Genet. (1989) 216:254-268
Lile
Nucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter capsulatus.
COSS-references MUID:89313663
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ion 05-Dec-1997
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                                    Score 944; DB 2; L. Pred. No. 1.10e-133; 24; Mismatches 11;
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#molecular-weight 17608
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benzodiazepine receptor/sensory t
- Archaeoglobus fulgidus
#formal_name Archaeoglobus fulgid
05-Dec-1997 #sequence_revision 05
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molecular-weight
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Matches 108; Conservative
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Similarity 37.2%;
'48; Conservative
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#length 169
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#length 160 (
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**Lorunan-rich sensory protein - Rhodobacter sphaeroides (strain 2.4.1)
#formal_name Rhodobacter sphaeroides
26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change
26-Jan-1996
A57438
A57438
Yeliseev, A.A.; Kaplan, S.
J. Biol. Chem. (1995) 270:21167-21175
A sensory transducer homologous to the mammalian peripheral-type benzodiazepine receptor regulates photosynthetic membrane complex formation in Rhodobacter sphaeroides 2.4.1.
A57438
D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          31 WYAGVEKPFFTPPNWLFGPAWTLLYFLIGIVLYIAW-E-NGFWNDSRVKATFFT-QLGLN
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Pred. No. 1.60e-32;
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#molecular-weight 17185
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#cross-references GB:AE000782;
#length 153 #molecu
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larity 39.0%;
Conservative
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38.3%;
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#length 158
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##residues 1-1
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##molecule_type DNA
##residues 1-1
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#common_name Chinese hamster
02-Jul-1996 #text_change
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         S49622 #type complete
crtK protein - Rhodobacter sphaeroides
#formal_name Rhodobacter sphaeroides
05-Mar-1995 #sequence_revision 12-May-1995 #text_change
09-Sep-1997
S49622
S49619
Lang, H.P.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N.
submitted to the EMBL Data Library, November 1994
In The complete DNA sequence, specific TNS insertion map and gene assignment of the carotenoid biosynthesis genes of Rhodobacter sphaeroides.
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I38724
Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krucz-Gene (1995) 155:201-205
Comparison of repetitive elements in the third in human and rodent mitochondrial benzodiazepine receptor-encoding genes.
receptor-encoding genes.
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mitochondrial benzodiazepine receptor
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3.98e-15;
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5.41e-27;
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8; NID:9575405;
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#formal_name Cricetulus griseus
02-Jul-1996 #sequence_revision (
28-Feb-1997
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Pred. No. 5
28; Mismat
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Pred. No. 3
2; Mismat
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larity 87.1%;
Conservative
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#length 31 #c
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#length 157
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#residues 1-3
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Borliss, R.; Boursier, L.; Brans, A.; Bruschi, C.V.; Caldwell, B.; Capuano, S.; Broulliet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, I.F.; Cummings, N.J.; Daniel, R.M.; Denizot, F.; Devine, K.M.; Doesterhoeft, A.; Ehrlach, S.D.; Emmerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fume, S.; Galizzi, A.; Galacron, J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Hennut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Raramata, D.; Kashbara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Konligstein, G.; Krogh, S.; Kumano, M.; Kutita, K.; Laddius, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel, C.; Medigue, C.; Medina, N.; Mellado, R.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwoll, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocho, B.; Rose, M.; Sadate, Y.; Sato, T.; Takahashi, H.; Terpstra, R.; Yoginde, S.; Sarot, P.; Shin, B.S.; Soldo, B.; Sorot, M.; Sadate, Y.; Sato, T.; Takahashi, H.; Terpstra, R.; Yoginda, M.; Tamawo, H.; Danchin, A.; Tamamoto, H.; Yamamoto, H.; Yamanot, R.; Yasamoto, K.; Yasamoto, K.; Yasamoto, K.; Yasamoto, M.; Yamanet, R.; Yasamoto, M.; Yamanet, R.; Yasamoto, R.; Yasamoto, R.; Yasamoto, R.; Yasamoto, R.; Yasamoto, R.; Yasamoto, M.; Yaname, H.; Danchin, A.; Yamamoto, H.; Yamanoto, H.; Yamanoto, H.; Yamanoto, H.; Yasamoto, R.; Yasamoto, R.
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                         hypothetical protein ytaB - Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_chang
05-Dec-1997
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Pred. No. 4.83e-08;
29; Mismatches 57
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RESULT

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de Wergifosse, P.; Jacques, B.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; Goffeau, A.
Yeast (1994) 10:1489-1496
The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome II reveals homologues to bacterial proline synthetase and murine alpha-adaptin, as well as a new permease and a DNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                PID:g1653694 EMBL Data
                                                                                      Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.

Ournal DNA Res. (1996) 3:109-136

Itle Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

ross-references MUID:97061201

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                     (PCC
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uracil transport protein homolog YBL042c - ye
(Saccharomyces cerevisiae)

protein YBL0406
#formal_name Saccharomyces cerevisiae
26-Aug-1994 #sequence_revision 09-Sep-1994 #t
21-Nov-1997
S45776; S50783
S45745
Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Sk
Wergifosse, P.; van Dyck, L.
submitted to the Protein Sequence Database, A
S45776
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                        sp.
S76477 *type complete
hypothetical protein - Synechocystis
#formal_name Synechocystis sp.
PCC 6803
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#residues 1-159 ##label KAN
#cross-references EMBL:D90915; NID:g1653604
#note the nucleotide sequence was :
Library, June 1996
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TITLE

ORGANISM
#formal_name Erwinia chrysanthemi
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24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change
21-Nov-1997
ACCESSIONS
C47755
REFERENCE
#authors
Lindeberg, M.; Collmer, A.
#journal
Analysis of eight out genes in a cluster required for pectic enzyme secretion by Erwinia chrysanthemi: sequence comparison with secretion genes from other gram-negative baccession
#status
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Lindeberg, M.; Collmer, A.
#status
#cross-references Muld and Secretion genes from other gram-negative bacteria.
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TG-QLALNWAWPPIFFGARQMGWALVDLLLVSGAAAATTVAWYQVS-PLAARLLYP-YLA
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##residues 1-639 ##label DEW
##cross-references EMBL:X78214; NID:g463261;
##experimental_source strain S288C
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transmembrane #
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.91 Seconds 613.189 Million cell updates/sec Tue Jul 21 14:54:08 1998; Run on:

not generated. output Tabular

Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 segs, 25083644 residues Searched

summaries Minimum Match 0% Listing first 45 Post-processing:

swiss-prot35 1:swiss1 Database:

scale 0.484 Variance 89.342; Mean 43.233; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

8	3.59e-203 1.94e-172 7.93e-171 1.48e-172 3.11e-171 2.22e-03 4.81e-01 5.01e-01 5.01e-01 1.17e+00 2.03e+00 2.03e+00 2.68e+00 3.51e+00	
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Score 1160; DB 1; Length 169; Pred. No. 3.59e-203;

99.18; 98.68;

Query Match Best Local Similarity

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EUKARYOTA; METAZOA; CHO
EUTHERIA; RODENTIA.
                                                                             SEQUENCE FROM N.A., ANI
TISSUE-ADRENAL GLAND;
MEDLINE; 90062173.
SPRENGEL R., WERNER P.,
GRAYSON D.R., GUIDOTTI
J. BIOL. CHEM. 264:204
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01-APR-1993 (REL.
01-NOV-1997 (REL.
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MOL. PHARMACOL. 45:201-211(1994).

CC -1- FUNCTION: RESPONSIBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE
BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE
BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXAMIDES.

CC MAY PLAY A ROLE IN THE TRANSPORT OF PORPHYRINS AND HEME.

CC -1- SUBCELLULAR LOCATION: MITOCHONDRION; INTEGRAL MEMBRANE PROTEIN.

CC -1- SIMILARITY: SEGMENTS TM1, TM4, AND TM5 SHOW SIMILARITY WITH THE TRANSMEMBRANE SEGMENTS M1, M2, AND M4 FROM SUBUNITS OF THE GABA(A)/BENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.

MGD; MGI: 88222; BZRP.

MITOCHONDRION; RECEPTOR; TRANSMEMBRANE

MITOCHONDRION; RECEPTOR; TRANSMEMBRANE

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TM2 (POTENTIAL).
TM3 (POTENTIAL).
TM4 (POTENTIAL).
TM5 (POTENTIAL).
TM5 (POTENTIAL).
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MEDLINE; 94158796.
GARNIER M., DIMCHEPAPADOPOULOS V.;
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EUTHERIA; R
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P16257;
01-AUG-19
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STRAIN=WISTAR;

MEDLINE; 93077057.

CASALOTTI S.O., PELAIA G., YAKOVLEV A.G., CSIKOS T., GRAYSON D.R.,

REUEGER K.E.;

GENE 121:377-382(1992).

-I- FUNCTION: RESPONSIBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE

BENZODIAZEPINE RECGNITION SITES AND IS MOST LIKELY TO COMPRISE

BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXAMIDES.

MAY PLAY A ROLE IN THE TRANSPORT OF PORPHYRINS AND HEMBE.

-I- SUBCELLULAR LOCATION: MITOCHONDRION; INTEGRAL MEMBRANE PROTEIN.

-I- SIMILARITY: SEGMENTS THI, TM4, AND TM5 SHOW SIMILARITY WITH THE

TRANSMEMBRANE SEGMENTS MI, M2, AND M4 FROM SUBUNITS OF THE

GABA(A)/BENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.

REMBL; J05122; G206162; -.

REMBL; J05122; G206480; -.

REMBL; M4221; G206480; -.

REMBL; M22880; A32680.

R PIR; JC1393; JC1393.

WMTOCHONDRION; RECEPTOR; TRANSMEMBRANE.
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                                                                                                                                                                                                                                                                              SANTI M.R
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                                                     (PKBS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e 1000; DB 1; L
l. No. 7.93e-171;
Mismatches 10;
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M2 (POTENTIAL).
M3 (POTENTIAL).
M4 (POTENTIAL).
M5 (POTENTIAL).
M5 (POTENTIAL).
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR)
BENZODIAZEPINE RECEPTOR).
BZRP OR MBR.
RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REL. 25, CREATED)
(REL. 25, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
YPE BENZODIAZEPINE RECEPTOR (PBR)
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                                                                                                                                         VERTEBRATA;
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METAZOA; CHORDATA; VERTEBRATA;
ARTIODACTYLA.
                                                                                                                                                                                                             SEQUENCE
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Pred. No. 7.
14; Mismato
                                                                                                                                                                                                                                                                                  I. M
K.E.
                                                                                                                                                                                                                                                                           TERNER P., SEEBURG P.H. GUIDOTTI A., KRUEGER K. 264:20415-20421(1989)
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                                                                               FUNCTION: RESPONSIBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXAMIDES. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: SEGMENTS TM1, TM4, AND TM5 SHOW SIMILARITY WITH THE TRANSMEMBRANE SEGMENTS M1, M2, AND M4 FROM SUBUNITS OF THE GABA(A)/BENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.
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SEQUENCE FROM N.A.
STRAIN-SB1003, AND BEC404;
MEDLINE; 89313663.
ARMSTRONG G.A., ALBERTI M., LEACH F., HEARST J.E.;
MOL. GEN. GENET. 216:254-268(1989).
-!- PATHWAY: CAROTENOID AND CHLOROPHYLL BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNE
(POTENTIAL).
-!- SIMILARITY: TO HUMAN MITOCHONDRIAL BENZODIAZEPINE RECEMBL; X52291; G46000; -.
EMBL; Z11165; G46125; -.
PIR; S04404; S04404.
PHOTOSYNTHESIS; CAROTENOID BIOSYNTHESIS; CAROTENOID BIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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CRIK.
RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).
PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE RHODOSPIRILLACEAE.
                                                      K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
11;
                                                      KRUEGER
                                                                                                                                                                                                                                                                                                                                                                                           M3 (POTENTIAL).
M4 (POTENTIAL).
M5 (POTENTIAL).
6E8EB394 CRC32;
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No. 1.48e-1
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LAST SEQUENCE UPI
LAST ANNOTATION I
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9
SEQUENCE FROM N.A.
MEDLINE; 91310699.
PAROLA A.L., STUMP D.G., PEPPERL D.J
LAIRD H.E. II;
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P17057;
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01-AUG-1990
01-OCT-1994
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P31711;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYPE 4 PREPILIN-LIKE PROTEIN SPECIFIC LEADER PEPTIDASE (ECOUTO.
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THE ALLANTOIN PERMEASE FAMILY
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P38196;
01-OCT-1994 (REL. 30, CREATED)
01-OCT-1994 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
PUTATIVE TRANSPORTER YBL042C.
YBL042C OR YBL0406.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                S
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I. No. 2.22e-03;
Mismatches 26
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FUNGI; ASCOMYCOTINA; HEMIASCOMYCETE
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                                                                                                                                                                                                                                                                                                                                   CE FROM N.A.

A=S288C;

A=S288C;

A=S288C;

EERGIFOSSE P., JACQL.
FEAU A.;

AST 10:1489-1496(1994).

1- SUBCELLUIAR LOCATION: INTA-
1- SIMILARITY: BELONGS TO THY
EMBL; X78214; G872301; -.
EMBL; X78214; G872301; -.
EMBL; X78214; G872301; -.
EMBL; Z35803; G536059; -.
PIR; S45776; S45776.

HYPOTHETICAL PROTEIN; TRAN

I TRANSMEM 163 180

TRANSMEM 2260 276

TRANSMEM 417 43

TRANSMEM 461 47

ANSMEM 461 47

ANSMEM 461 47

ANSMEM 461 47

ANSMEM 484

S39 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.8%;
larity 26.2%;
Conservative
Similarity 37.2%; 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 22; Conser
                                                                                                                                                                              160
                                                                                                                                                    154
                                                                                                                                                                            YCVWRDNHG
                                                                                                                                                  FSVWRLNPG
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EMBL;
EMBL;
EMBL;
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Matches
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                        RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLTJ.
ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12;
MEDLINE; 97061202.
OSHIMA T., AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A.,
IKEMOTO K., INADA T., ITOH T., KAJIHARA M., KANAI K., KASHIMOTO K.,
KIMURA S., KITAGAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K.,
MORI H., MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., SAITO N.,
SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O.
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                                                                SEQUENCE FROM N.A.
STRAIN-EC16;
MEDLINE; 93054355.
LINDEBERG M., COLLMER A.;
J. BACTERIOL. 174:7385-7397(1992).
-!- FUNCTION: CLEAVES TYPE-4 FIMBRIAL LEADER SEQUENCE AND METHYLATES THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE (PROBABLE).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C20; ALSO KNOWN AS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K., DUNCAN M.,
                        ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLASNER
                                                                                                                                                                                                                                                                                               TRANSMEMBRANE; INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ന
                                                                                                                                                                                                                            C20; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGAW-LGWQALPNLVLIASLTGLTATLLWQRIHRLSMQQPLAFGPWLAVSGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLTJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHUNG E., ALLEN E., ARAUJO R., APARICIO A., DAVIS K., DUN FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O., LE NAMATH A., OEFNER P., ROBERTS D., SCHRAMM S., DAVIS R.W.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                      FACULTATIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., PERNA N.T
DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                III LEADER PEPTIDASE FAMILY C2

III LEADER PEPTIDASE FAMILY.

(BL; LO2214; G148444; -
R; C47755; C47755.

DROLASE; PROTEASE; TRANSPORT; TRANSMEMBRANE;
ANSMEM 13 33 POTENTIAL.
ANSMEM 126 POTENTIAL.
ANSMEM 153 173 POTENTIAL.
ANSMEM 153 173 POTENTIAL.
ANSMEM 176 196 POTENTIAL.
ANSMEM 259 279 POTENTIAL.
ANSMEM 259 279 POTENTIAL.
ANSMEM 259 279 POTENTIAL.
ANSMEM 259 279 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.81e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUTAMATE/ASPARTATE TRANSPORT SYSTEM PERMEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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EMBL/GENBANK/DDBJ
                  SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105;
Pred. No. 4
23; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.0%;
larity 26.4%;
Conservative
ERWINIA CHRYSANTHEMI.
PROKARYOTA; GRACILICUTES;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | FROM N.A.
| 12 / MG1655;
| F.R., PLUNKETT (
| D (JAN-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
F
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STRAIN-K12 / BK9MDG;
LUM D., WALLACE B.J.;
SUBMITTED (JUN-1994) T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
14; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EN A
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P41074;
01-FEB-1995
01-FEB-1995
01-NOV-1997
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STRAIN-K12
BLATINER F.
                                                                                                                                                                                                                                                                                           HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED
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TRANSMEM
TRANSMEM
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TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220
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Best I
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RARRAR REPRESENTATION OF THE PROPERTY OF THE P
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RODS
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                                                                                          MEMBRANE
                                                                                                                                THE HISMO
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                                                                                                                                    PROTELL.
SUBFAMILY.
SUBFAMILY.
SUBFAMILY.
EMBL; U10981; G624630; -.
EMBL; U2598; G1778572; -.
EMBL; D90705; G1651273; -.
EMBL; D90706; G1651273; -.
TRANSMEM 33 53 POTENTIAL.
TRANSMEM 74 94 POTENTIAL.
TRANSMEM 104 124 POTENTIAL.
TRANSMEM 104 124 POTENTIAL.
TRANSMEM 212 233 POTENTIAL.
TRANSMEM 212 233 POTENTIAL.
TAANSMEM 213 POTENTIAL.
TAANSMEM 33 53 G8
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Γ.
                              SY
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                            TRANSPORT
OR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAV
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                                                                                          INNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE FRAMESHIFTS.
L; AE000142; G1786549; -.
L; U73857; G1657549; -.
L; D85613; -; NOT_ANNOTATED_CDS.
RES. 3:137-155(1996).
FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRAFOR ASPARTATE/GLUTAMATE; PROBABLY RESPONSIBLE FOR TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCOTOBACTERIA; FACULTATIVELY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESULT 9

D MHPT_ECOLI STANDARD; PRT; 418 AA.

2 P77589; P77037;

01-NOV-1997 (REL. 35, CREATED)

01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

PUTATIVE 3-HYDROXYPHENYLPROPIONIC ACID TRANSPORTER.

ESCHERICHIA COLI.

PROKARYOTA: CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.M., CHUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., DAVIS R
DATA BANKS.
                                                                                                                                  Ö
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DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEL-LVSGAAAATTVAWYQVSPLAARLL-YPYLAWLAFTT-TLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMMNLVKNSAIASTIGLVDMAAQAGKLLDYSAHAWESFTAITLAY
                                                                                                                              COMPONENTS
                                                                                                                             INTEGRAL MEMBRANE COMPONENTS TRANSPORT SYSTEMS. BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATA
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EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLEN E., ARAUJO R., APARICIO P. N., HYMAN R., KALMAN S., KOMP COEFNER P., ROBERTS D., SCHRAMM (NOV-1996) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H., SAITO N.;
(MAY-1996) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 98-345 FROM N.A.
STRAIN-K12 / CS520;
FERRANDEZ A., GARCIA J.L., DIAZ E.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ
-! - FUNCTION: COULD BE A TRANSPORTER FOR 3
(HYDROCINNAMIC ACID).
-! - SUBCELLULAR LOCATION: INTEGRAL MEMBRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
BLATTNER F.R., PLUNKETT
SUBMITTED (JAN-1997) TO
                                                                                                       (PROBABLE).
SIMILARITY: WITH |
PROTEIN-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12;
NASHIMOTO H., SAIT
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DUNCAN M.,
FEDERSPIEL
NAMATH A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CDP-DIGLYCERIDE (CDP-DIACYLGLYCEROL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
EMBL; D50811; G1262332; -.
TRANSFERASE; NUCLEOTIDYLTRANSFERASE; PHOSPHOLIPID BIC
TRANSMEM 12 32 POTENTIAL.
TRANSMEM 53 73 POTENTIAL.
TRANSMEM 111 131 POTENTIAL.
TRANSMEM 136 156 POTENTIAL.
TRANSMEM 136 156 POTENTIAL.
TRANSMEM 136 156 POTENTIAL.
TRANSMEM 136 156 POTENTIAL.
TRANSMEM 174 194 POTENTIAL.
TRANSMEM 174 194 POTENTIAL.
TRANSMEM 251 271 POTENTIAL.
TRANSMEM 251 271 POTENTIAL.
TRANSMEM 251 271 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OHTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGFFLLEGAFFALFIGAVVSLGAWEWARLAGYEQQFGR--VAY-
                                                                                                                                SYMPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
E CYTIDYLYLTRANSFERASE (EC 2.7.7.41)
(CDP-DIGLYCERIDE PYROPHOSPHORYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    • •
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REF. 4
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
11e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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. No. 5.01e-C
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 100; DB 1
Pred. No. 2.11e-
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: PHOSPHOLIPID BIOSYNTHESIS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KURODA A., KATO J.
EMBL/GENBANK/DDBJ DI
CTP + PHOSPHATIDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197543; E242997; -.
1; EG13293; MHPT.
1; PS00216; SUGAR_TRANSPORT_1; 1.
1; PS00217; SUGAR_TRANSPORT_2; 1.
1; PS00217; SUGAR_TRANSPORT_2; 1.
1; PS00217; SUGAR_TRANSPORT_1; 1.
1; PS00217; SUGAR_TRANSPORTINIAL.
1; PS00217; SUGAR_TRANSPORTENTIAL.
1; PS00217; SUGAR_TRANSPORTENTIAL.
1; PS00217; SUGAR_TRANSPORTENTIAL.
1; PS00216; SUGAR_TRANSPORT_1; 1.
1; PS00216; SUGAR_TRANSPORTENTIAL.
1; PS00216; SUGAR_TRANSPORTENTIAL.
1; PS00217; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
24; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGAALAATLGFAGANLAWQTV
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27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5%;
larity 26.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AERUGINOSA.
GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PAO1;
TAGUCHI K., FUKUTOMI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (APR-1996) TO
-!- CATALYTIC ACTIVITY:
CDP-DIACYLGLYCEROL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSA_PSEAE STAL
059640;
01-NOV-1997 (REL.
01-NOV-1997 (REL.
01-NOV-1997 (REL.
PHOSPHATIDATE CYTI
SYNTHETASE) (CDP-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDSA OR CDS.
PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
SA_PSEAE
59640;
         EMBL; X975
ECOGENE; E
PROSITE; P
PROSITE; P
TRANSPORT;
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SEQUENCE
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Best Loc
Matches
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Best Loc
Matches
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            SET THE FEET HER SOLVER SOLVER
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3
                                                                                                                                                                                                                                                                                                                (G6-AMYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

-1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.

-1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

-1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.

-1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.

EMBL; U25817; G870784; -.
                                                                                                                                                                                                                                                                                                                                                                                BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.

MEDLINE; 88162814.

TSUKAMOTO A., KIMURA K., ISHII Y., TAKANO T., YAMANE K.;

BIOCHEM. BIOPHYS. RES. COMMUN. 151:25-31(1988).

-1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC LIN

MALTOHEXAOSE RESIDUES FROM THE NON-REDUCING CHAIN ENDS.

-1- PATHWAY: DEGRADATION OF STARCH.

-1- SUBCELLULAR LOCATION: EXTRACELLULAR.

-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALS

KNOWN AS THE ALPHA-AMYLASE FAMILY.

EMBL; M18862; G142497; -.

PIR; A27705; A27705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
ب
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                                                                                                                                                                                                                           UI-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE PRECURSOR (EC 3.2.1.98)
(MALTOHEXAOSE-PRODUCING AMYLASE) (EXO-MALTOHEXAOHYDROLASE)
BACILLUS SP. (STRAIN 707).
PROKARYOTA; FIRMICUTES; ENDOSPOPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALTOHEXAOSE-PRODUCING AMYLAS:
FB2B65AE CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FD3C_SESIN STANDARD; PRT; 447 AA.
P48620;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. 4294; TISSUE-COTYLEDON;
SHOJI K.;
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Le..
5.01e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYDRATE METABOLISM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIENTAL SESAME) (GINGELLY).
(A; EMBRYOPHYTA; ANGIOSPERMAE; PEDALIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108
                                                                LPQLAGAVLLLALVWWTLATVLVL-TYPESVGYWGGRW
                                                                                          :: ||: :| | ::| | ::|| VSPLAARLYPYLAWLAFTTTLNYCVWRDNHGWRGGRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 WI-PPAWKGASQNDVGYGAYDLY-DLGEFNQKGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518
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Pred. No.
9; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOSIDASE; CARBOHY
1 33
34 518 M
518 AA; 59009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%;
larity 37.1%;
Conservative
                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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SCROPHULARIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESAMUM INDICUM
                                                                                                                                                                       LT 11
AMT6_BACS7
P19571;
01-FEB-1991
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
CHAIN
SEQUENCE
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4;
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                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- YHISFPVLSRSSFGTWGSLWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE;
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                                                                                                                              ••
                                                                                                                            4
                      AST (POTENTIAL).
FATTY ACID DESATURA
                                                                                                                                                16
                                                                                                       Length 447
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                       NE PROTEIN.
PERMEASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indel
 CHLOROPLAST;
                                                                                                                                                            WRSMG-YVVRDVAVVFGLAAVAAYFNNWVVWPLYWFAQSTMFWALFVL
                                                                                                                                                                                                                                                                                                                                                   DATA BANKS
                                                                                                                                                                                                                                                                                                                               ф
                                                                                                                                                                                                                                                                                                                              KAMMERER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 95; DB 1; Len ... No. 8.83e-01; Mismatches 26;
                                                                                                                            ö
                                                                                                                                                                                                                                                                                    SS POMBE (FISSION YEAST).
ASCOMYCOTINA; HEMIASCOMYCETES
                     CHLOROPLAST (POTEI OMEGA-3 FATTY ACII CHLOROPLAST. HISTIDINE BOX 1. HISTIDINE BOX 2. HISTIDINE BOX 3. ; 67B2C46B CRC32;
                                                                                                                  -01
                                                                                                                                                                                                                                                                                                                        CHEVALLIER M.R., STRAUB M.L., BACH M.L., KAMMER CHEVALLIER M.R., STRAUB M.L., BACH M.L., KAMMER DE MONTIGNY J.;

SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA -!- FUNCTION: TRANSPORT OF URACIL.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO-!- SIMILARITY: BELONGS TO THE ALLANTOIN PERMER BABL; X98696; E251596; -.

TRANSMEM 62 82 POTENTIAL.

TRANSMEM 143 163 POTENTIAL.

TRANSMEM 252 272 POTENTIAL.

TRANSMEM 252 272 POTENTIAL.

TRANSMEM 342 362 POTENTIAL.

TRANSMEM 342 362 POTENTIAL.

TRANSMEM 407 427 POTENTIAL.

TRANSMEM 407 427 POTENTIAL.

TRANSMEM 461 481 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC32
                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .. 27, CREATED)
.. 35, LAST SEQUENCE UPDATE)
.. 35, LAST ANNOTATION UPDATE)
PROTEIN.
                                                                                                       DB 1;
8.83e-
                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELGLNW-WEA-WICVW-VGY-LICGILVATTGRPGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
  BIOSYNTHESIS;
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Pred.
24; M
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  ACID
                                                                                                      Similarity 33.3%;
16; Conservative
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21; Conservative
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207
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P32784; Q07062;
01-OCT-1993 (REL.
01-NOV-1997 (REL.
01-NOV-1997 (REL.
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(REL.
(REL.
                                                                                                                                                                                                                                                                                              EUKARYOTA; FUNGI;
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                                                    167
203
370
OXIDOREDUCTASE;
             PEPTIDE
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FUR4_SCHPO
Q10279;
01-NOV-1997
01-NOV-1997
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Best Local S
Matches 2
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            TRANSIT
TRANSIT
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DOMAIN
DOMAIN
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Best Loc
Matches
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- CONTAINING
PROTEIN
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                                                                                                                                                                                                                                                         SEQUENCE OF 609-759 FROM N.A.

STRAIN=S288C;

MEDLINE; 93070613.

DELAVEAU T., JACQ C., PEREA J.;

YEAST 8:761-768(1992).

-1- FUNCTION: MULTICOPY SUPPRESSOR OF THE CTR1 MUTATION.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).

-1- SIMILARITY: STRONG, TO YEAST YRR067W.

EMBL; 235773; G535999; -.

EMBL; S47695; E65046; -.

PIR; S25330; S25330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIF4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMPHIBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE; 95180446.

WAKIYAMA M., SAIGOH M., SHIOKAWA K., MIURA K.I.;

FEBS LETT. 360:191-193(1995).

-1- FUNCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE- CONT
MRNA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTE
SYNTHESIS AND FACILITATES RIBOSOME BINDING BY INDUCING THE
UNWINDING OF THE MRNAS SECONDARY STRUCTURES.

-1- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, EIF4G AND EI

(WHICH CAN CYCLE IN AND OUT OF THE COMPLEX).

EMBL; D31837; G849076; -.

EMBL; D31837; G849076; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \mathbf{c}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YQEPSATKKILYSIATWLLYNI-FH-CFFREIRG-RGSFKVPQ
OR YBL011W OR YBL0315 OR YBL0309.
HAROMYCES CEREVISIAE (BAKER'S YEAST).
RYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e 94; DB 1; L
. No. 1.17e+00;
Mismatches 12
                                                                                                                                                                                                           GOFFEAU A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REF. 2
REF. 2
REF. 2
REF. 2
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TET
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Pred.
16; M
                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-S288C;
MEDLINE; 93070615.
SKALA J., VAN DYCK L., PURNELLE
YEAST 8:777-785(1992).
                                                [1]
SEQUENCE FROM N.A.
MEDLINE; 95332274.
MATSUSHITA M., NIKAWA J.;
J. BIOCHEM. 117:447-451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
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larity 27.9%;
Conservative
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                  SACCHAROMYCES CEREVI.
EUKARYOTA; FUNGI; AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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IF4E_XENLA
P48597;
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INITIATION FACTOR; PROTEIN BIOSYNTHESIS; RNA-BINDING. SEQUENCE 213 AA; 24635 MW; 4F60C133 CRC32;
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. 9 Score 92; DB 1; Length 213; Pred. No. 2.03e+00; 18; Mismatches 47; Indels Query Match Best Local Similarity 25.3%; Matches 24; Conservative

Gaps

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Search completed: Tue Jul 21 14:54:26 1998 Job time: 18 secs.

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protein - protein database search, using Smith-Waterman algorithm MasPar time 12.32 Seconds 577.651 Million cell updates/sec Tue Jul 21 14:54:44 1998; MPsrch_pp Run on:

not generated. output Title: Description: Perfect Score: Sequence:

Tabular

Scoring table:

42109429 residues PAM 150 Gap 11

140542 seqs,

Searched:

summaries Minimum Match 0% Listing first 45 Post-processing

Database:

sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

scale 0.444 Variance 94.668; Mean 42.037; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ed.	.27e-15	.01e-1	.96e-36	.02e-2	.72e-2	.88e-1	.49e-0	,21e-0	.55e-0	.58e-0	.58e-0	.21e-0	þ	.16e-0	٦.	. 21	0	.40e	1.40e+00	.83e+0
ion	ENZODIAZEPINE RECEPT	RIPHERAL BENZODIAZE	OCHONDRIAL BENZODI		ICAL PROTEIN	MITOCHONDRIAL BENZODIA	IN.	YPOTHETICAL 17.8 KD	YPOTHETICAL 69.	UTATIVE GTG START CO	OTHETICAL 32.	YOAV.	SS I PROTEI	LASTID OMEGA-3 FATTY	-15 LINEOYL DES	THETICAL 57.1 KD	HETICAL 21.6 KD	HETICAL 40.5 KD	-3 FATTY AC	ERASE (FRAG
ID	6211	385	2879	5479	9336	6041	3469	7450	5546	4538	7351	3441	030838	2380	4011	7187	0663	580	480	955
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WUG, FWUD AND	COTHETICAL 35.9 K	ATTY ACID DESATURASE	Y ACID DESATURA	YKVW PROTEIN.	FATTY ACID DE	POTHETICAL 64.	ROME	S-LIPOXYGENASE	SE	SENSORY TRANSDUCTION H	POTHETICAL 12.4 KD	NADH DEHYDROGENASE SUB	ICAL 57.1	ETICAL 36.6 KD	PRE S1/S ORF.	ATE MEMBRANE	H	99	E PROTEIN	M BASES 1676082 TO	SIMILAR TO LIGAND-GATE	S PROTE	E PR
P94945	9513	2462	2382	3168	9335	1403	311	1529	9315	2646	3293	2140	5517	7343	6787	7754	1329	7610	6795	7742	9119	4174	839
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96																							
21																							

ALIGNMENTS

SUI	DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-TAN-1999 (TREMBLREL. 06, 1957 ANNOWARD)	BENZODIAZEPINE RECEPTOR, PER RECEPTOR).	GN BZRP.	EUKARYOTA; ME			STRAIN-BALB/C;	RA TAKETANI S., KOHNO H., OKUDA M., FURUKAWA T., TOKUNAGA R.; RI. T. BIOL, CHEM 269-2527-7531/1994/	EMBL; D21207; G	88222; BZRP.	SEQUENCE	Query Match Best Local Similarity 83.2%; Pred. No. 4.27e-156; Matches 119; Conservative 14; Mismatches 10; Indels 0; Gaps	Db 27 RGEGLRWYASLOKPSWHPPRWTLAPIWATLYSAMGYGSYIVWKELGGFTEDAMVPLGLYT 86	QY 27 HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYT 86	DD 87 GQLALNWAWPPIFFGARQMGWALADLLLVSGVATATTLAWHRVSPPAARLLYPYLAWLAF 146	OY 87 GOLALNWAWPPIFFGAROMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAF 146	VLNY YVWRDNS	QY 147 TTTLNYCVWRDNHGWRGGRRLPE 169	$\bar{\mathbf{o}}$	AC Q13850; DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
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KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZHOU L.,
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
MITOCHONDRIAL BENZODIAZEPINE RECEPTOR/SENSORY TRANSDUCTION PROTEIN
AF1475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON.K.E.,
KEENK H.P., CLAYTON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOI
OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T
COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FULGIDUS.
                                                      TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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(DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BANKS
                                                                                                                                                                                                                                                                                                                                                                                                      e 956; DB 2; L
. No. 7.01e-149;
Mismatches 9;
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                                                                                                                                                                                                                    3
                                                   CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                    MILLER
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                                                                                                                                                                                                                                                                                                                                                                                                Score 956;
Pred. No. 7
7; Mismat
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PERIPHERAL BENZODIAZEPINE RECEPTOR HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                    J.F.,
                                                                                                                           SEQUENCE FROM N.A.

TISSUE-PLACENTA;

MEDLINE; 94140364.

LIN D., CHANG Y.J., STRAUSS J.F.

GENOMICS 18:643-650(1993).

EMBL; L21954; G488425; -.

EMBL; L21952; G488425; JOINED.

EMBL; L21953; G488425; JOINED.

SEQUENCE 169 AA; 18483 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                  th 81.7%;
Similarity 86.2%;
125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G2649094;
AA; 17185
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AE001001; G264
NCE 153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCHAEOGLOBUS FU
ARCHAEBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VENTER J.C.;
SUBMITTED (N
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SUBMITTED
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Best Local S
Matches 12
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SEQUENCE
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                                                  WYAGVEKPFFTPPNWLFGPAWTLLYFLIGIVLYIAW-E-NGFWNDSRVKATFFT-QLGLN
                                                                                                              WYAGLOKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYTGQLALN
                                                                                                 FLWSILFFGLQNPLA-GLVDIIALDIAVILTIVYIYHHSK-ASLLLLPYLGWILFASALN
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MEDLINE; 94150718.
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A:, MORTIMORE B.,
                                                                                                                                                                                                                                                                                                           RHODOBACTER SPHAEROIDES (RHODOPSEUDOMONAS SPHAEROIDES).
PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA
RHODOSPIRILLACEAE.
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 153;
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01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
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(TREMBLREL. 05, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
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U
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 291; DB 9; L4
Pred. No. 1.02e-29;
28; Mismatches 42;
Score 327; DB 9; L. Pred. No. 8.96e-36; 30; Mismatches 39;
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STRAIN-NCIB 8253;
MEDLINE; 95238278.
LANG H.P., COGDELL R.J., TAKAICHI S.J., BACTERIOL. 177:2064-2073(1995).
EMBL; X82458; G575409; -.
SEQUENCE 157 AA; 17854 MW; D56D
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larity 36.7%;
Conservative
27.9%;
larity 39.0%;
Conservative
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(TREMBLREL.
(TREMBLREL.
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O93367;
O1-FEB-1997 (TREMBLREL.
O1-JAN-1998 (TREMBLREL.
O1-JAN-1998 (TREMBLREL.
HYPOTHETICAL PROTEIN C41
C41G7.3.
CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (OCT-1996)
            Similarity
48; Conser
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est Local Similarity
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Q54791
Q54791;
01-NOV-1996
01-NOV-1996
CRT GENES.
                                                                                                                                                  148
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STEWARD C
 Query Match
Best Local S
Matches 4
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Best Loc
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S P., BOLOTIN A., BORCHERT S.,
BRAUN M., BRIGNELL S.C., BRON
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   ROOPRA A.,
SONNHAMMER
, VAUDIN M.
                                                                                                                                                             Length 553;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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ANNOTATION UPDAT
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O60419;
O60419;
O1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE MITOCHONDRIAL BENZODIAZEPINE RECEPTOR (FRAGMENT)
                                                                                                                                                           Score 245; DB 3; L. Pred. No. 3.72e-22; 32; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·- C
O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L. SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A. STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK WILKINSON-SPROAT J., WOHLDMAN P.; NATURE 368:32-38(1994).
EMBL; Z81048; E348255; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 10;
9.88e-17;
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CHORDATA; VERTEBRATA;
                                                                                                                              A2548F6C
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BERTERO M.G., BESSIERES P.,
BOURSIER L., BRANS A., BRAU
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Pred. No.
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STRAIN-168;
KUNST F., OGASAWARA N., MOS
AZEVEDO V., BERTERO M.G., B
BORRISS R., BOURSIER L., BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.0%;
larity 87.1%;
Conservative
                                                                                                                                                           Similarity 35.7%; 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAKOVLEV A.G., RUFFO M., GENE 155:201-205(1995).
EMBL; U12420; G529944; -.
NON_TER 1 1 1
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(TREMBLREL.
(TREMBLREL.
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                                                                                                            HYPOTHETICAL PROTEIN.
SEQUENCE 553 AA; 6
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EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                     158
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hes 27; Conse
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034694
034694;
01-JAN-1998 ('01-JAN-1998 ('YTAB PROTEIN.
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PROKARYOTA;
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MEDLINE;
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Matches
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BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
A FRITZ C., FUJITA M., FUJITA Y., FABRET C., FALLIZZI A., GALLERON N.,
GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
A HILBERT H., HOLSAPPEL S., HAGONO S., HULLO M.F., ITAYA M., JONES L.,
JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
A NOBYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NARAI S., NOBACK M.,
NOONE D., O'REILLY M., OGAWA K., OGUDEGA B., PARK S.H.,
PARKO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M.,
PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
A REGER M., RIVOLTA C., RCCHA E., ROCHE B., RASPARIU E.,
SATO T., SCANLAN E., SCHIEICH S., SERROR P., SHIN B.S., SOLDO B.,
SOROKIN A., TACCONI E., TANAGI T., TAKEMARU K.,
TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
TANENCHI M., TAMAKOSHI A., YANAHE F., VASSAROTTI A.,
VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENEGGER T.,
NITRERS P., WIRPAT A., YANAMOTO K., YASUMOTO K., YASUMOTO K., YASUMOTO K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                  В.
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             N.J., DANIEL A...
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LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z99119; E1185966; -.
EMBL; AF008220; G2293285; -.
EMBL; AF008220; G2293285; -.
SEQUENCE 155 AA; 17288 MW; 875DAD85 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
HYPOTHETICAL 17.8 KD PROTEIN.
SYNECHOCYSTIS SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 160; DB 9; LAPred. No. 5.49e-09; 29; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G., VENEMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.M., BELDMAN G
11:203-218(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF 119-155 FROM N.A. 94195107.
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larity 27.9%;
Conservative
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KIEL J.A., BOELS
MOL. MICROBIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ET 8
P74502
P74502;
01-FEB-1997
01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TI 150
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STRAIN=168;
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Best Local
Matches
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C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153
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137
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                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                        LRWFNRLRRPSWLTFEWAIPFIWIAIFIAGAISATLAWNATADPGHRWGLMVGYLLLELT
                                                                                                                                                                                   VM-AYTPVMCKLRSLRVGSIIGATGFFVGLALVIAVS--QVSTTAFGFLVPFLLWSPIGT
                                                                                                                                                                                                                          LNWAWPPIFFGAR--OMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAFTT
                                                    NAKAMURA
                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND COCCI
                                                                                                                                                                                                                                                                                                                                                                                                  T., MIYAJIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                        SEQUENCE FROM N.A.
STRAIN-PCC6803;
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M., TABATA S.;
DNA RES. 3:109-136(1996).
EMBL, D90915; G1653694; -.
                                                                                                                                            Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 634;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 LWNRMPVTTTSFVVGSAGLLAVFPLGMFWTWQKWFSGDWLVSWPLLALLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEROBIC RODS
                                                                                                                                                                                                                                                                                    (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                      Score 130; DB 9; L. Pred. No. 9.21e-05; 30; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                 SAZUKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
           EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 9; 1
1.55e-01;
                                                                                                                      9EA93412 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                            8CEC37CB CRC32;
                                                                                                                                                                                                                                                                       A.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z
                                                                                                                                                                                                                                                                                                                                                                                              S., KOTANI H.,
                                                                                                                                                                                                                                                                      634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BORDETELLA PERTUSSIS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 105;
Pred. No. 1
14; Mismat
                                                                                                                                                                                                                                                      OS5465
OS5465
OS5465;
O1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQU)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQU)
HYPOTHETICAL 69.4 KD PROTEIN.
SLL0026.
SYNECHOCYSTIS SP.
PROKARYOTA; BACTERIA; GRACILICUTES; O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                    17809 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          69363 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TREMBLREL. 01,
(TREMBLREL. 01,
(TREMBLREL. 01,
G START CODON.
                                                                                                                                       11.1%;
25.0%;
                                                                                                                                                                                                                                                                                                                                             CHROCCCALES.
[1]
SEQUENCE FROM N.A.
STRAIN=PCC6803;
MEDLINE; 96127529.
KANEKO T., TANAKA A., SATO
SUGIURA M., TABATA S.;
DNA RES. 2:153-166(1995).
EMBL; D64006; G1001322; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 634 AA; 69363 M
                                                                                                                                              Similarity 25.08, 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               SATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match
Local Similarity 30.0%;
les 15; Conservative
            P
O
TABATA S.;
SUBMITTED (JUN-1996)
                                                                                                                   159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM 1
STRAIN-BP536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROKARYOTA; GR
ALCALIGENACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q45384;
Q45384;
O1-NOV-1996 (
O1-NOV-1996 (
O1-NOV-1996 (
PUTATIVE GTG
BPLJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTG
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Local S
                                                                                                                   SEQUENCE
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACILLACEAE
                                                                                                                                                                                            Gaps
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SEQUENCE FROM N.A.

STRAIN=PCC6803;

L SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

[2]

SEQUENCE FROM N.A.

STRAIN=PCC6803;

KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,

MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,

A MIYAJIMA N., HIROSAWA M., TANAKI A., NAKAZAKI N., NARUO K.,

A HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,

A OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,

L DNA RES. 3:109-136(1996).

E EMBL; D90907; G1652634; -.

HYPOTHETICAL PROTEIN.

SEQUENCE 285 AA; 31950 MW; BE7A9038 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \rightarrow
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                                                                                                                                          Length
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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TO EMBL/GENBANK/DDBJ DATA BANK
                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBLREL. 02, CREATED)
(TREMBLREL. 02, LAST SEQUENCE UPDATE)
(TREMBLREL. 02, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
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1. No. 3.58e-01;
Mismatches 23;
                                                                                                                               Score 102; DB 9;
Pred. No. 3.58e-01
10; Mismatches 1
                                                                                      CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROOCOCCALES;
                                                                                                                                                                                                                                                                                    52
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                                                                                  F6C7644C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102;
Pred. No. 3
24; Mismat
                                                                                                                                                                                                                                                      | || :::|: || :::
|TIVAWYQVSPLAARLLYPYLAWLAFTTTLNY
                                                                                                                                                                                                                            TGGVWYNINDMATALVFANLIWLLIKRKLSF
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
ALLEN A.G., MASKELL D.J.;
MOL. MICROBIOL. 19:37-52(1996)
EMBL; X90711; G992979; -.
SEQUENCE 188 AA; 21467 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPEVSFHHLENGSLLVFALFMLTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PP-IFFGARQMGWALV-DLLLVSGA
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                             Query Match
Best Local Similarity 29.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLGP.
SYNECHOCYSTIS SP.
EUBACTERIA; CYANOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%;
larity 30.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05,
05,
05,
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(TREMBLREL.
(TREMBLREL.
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A; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . N
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LAPIDUS A., GALLERON
SUBMITTED (NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
OGASAWARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
STRAIN-168;
KUNST F., OGASAWAR.
                                                                                                                                                                                                                                                                                                                                               LT 11
P73514
P73514;
01-FEB-1997 (01-FEB-1997 (01-FEB-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             034416;
01-JAN-1998
01-JAN-1998
01-JAN-1998
YOAV.
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                                                                                                                            Query Match
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Best Local S
Matches 2
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034416
034416;
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I., ALBERTINI A.M., ALLONI

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A AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS R., BOURSIER L., BRANS A., BRADN M., BRIGNELL S.C., BRON S.,
BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
ENTIZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
GHISEPII G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HERADT A.,
HILBERT H., HOLSAPPEL S., HAGSONO S., HULLO M.F., ITAYA M., JONES L.,
A HILBERT H., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
A KOBAYASHI Y., MOETLEY P., KONINGSTEIN G., KROGH S., KUMANO M.,
A HELBER K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
A HELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
A PARRO V., POHL T.M., PORTETELLE D., PORMOILIK S., PRESCOTT A.M.,
PRESECAN E., PUJIC P., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
SAHO T., SCANLAN E., SCHLEICH S., SCHEDETER R., SCOFFONE F.,
SEKIGGCHI J., SEKOWSKA A., SEROR S.J., SERROR P., THERBARU K.,
TAMAROSHI A., TAMAROSHI A., TAKAHASHI H., TAKEMARU K.,
TAMAROCHI M., TAMAROSHI A., VIRDI B.S., VOGNONI A.,
TAKEUCHI M., TAMAROSHI A., VIRDI B. MATTATTATTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    DANCHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 SAEWIYQAVWSLLFNGLLSTGFTFVVWFWVLNQIQASKASMAL-MFVPVLALFFGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPHWVLGPVWGTLYSAM-GYG-SYLVW-KELGGF-TEKAVVPLGLYTGQLALNWAW
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                                                                                                                                                                                                                                                                                                                                                                                   VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENEGGER T., WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHNATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AF027868; G2619001; -.
EMBL; 299114; E1185349; -.
SEQUENCE 292 AA; 33044 MW; 2CD69019 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100; DB 9; Lour Pred. No. 6.21e-01; 19; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۰- م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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Pred. No. 6.
5; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 90375196.
GROSSBERGER D., HEIN W.R., MARC
IMMUNOGENETICS 32:77-87(1990).
EMBL; M34676; G166002; -.
PROSITE; PS00290; IG_MHC; 1.
SIGNAL; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TREMBLREL. 01, LA
(TREMBLREL. 05, LA
PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S (SHEEP).

METAZOA; CHORDATA;
ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41442 MW;
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larity 40.0%;
Conservative
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18; Conser
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29
368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   030838;
01-NOV-1996
01-NOV-1996
01-JAN-1998
MHC CLASS I
OVIS ARIES (;
EUKARYOTA; MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FRC
STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL; N
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                51 WSSMG-YVVRDVVVVLALAATAARLDSWLAWP-VYWAAQGTMFWALFVLGHDCGHGSFSN
                                                                                                                                                                                                                                                                                                            MAGNOLIOPSIDA;
                                                                                                                                                                                         Ξ
                                                                                                                                      MONOCOTYLEDONEAE
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6
                                                                                                                                                                                         NISHIMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112
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         9
         N
                                                                                                                                                                                                                                                        Length
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                                      O23802 PRELIMINARY; PRT; 380 AA.
O23802;
O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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e-01;
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBRYOBIONTA; MAGNOLIOPHYTA; LIMNANTHACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                            TAFAD7.

TAFAD7.

TRITICUM AESTIVUM (WHEAT).

EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MO
CYPERALES; GRAMINEAE.

[1]

SEQUENCE FROM N.A.

STRAIN-CV. CHIHOKU; TISSUE-LEAF;
HORIGUCHI G., IWAKAWA H., KODAMA H., KAWAKAMI N.

PHYSIOL. PLANTARUM 96:275-283(1996).

EMBL; D43688; D1008371; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e 99; DB 8; L
|. No. 8.16e-01;
| Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327D77FE CRC32;
                                                                                                                                                                                                                                   CRC32
                                                                                                                                                                                                                                                      e 99; DB 8;
I. No. 8.16e-
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         436
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Pred. No.
11; Misma
                                                                                                                                                                                                                                                      Score 99;
Pred. No.
17; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 95334518.
BHELLA R.S., MACKENZIE S.L.;
PLANT PHYSIOL. 108:861-861(1995)
EMBL; U17063; G699390; -.
SEQUENCE 436 AA; 50093 MW; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :55:36
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O40118;
O40118;
O1-NOV-1996 (TREMBLREL. 01, CI
01-NOV-1996 (TREMBLREL. 01, LJ
01-NOV-1996 (TREMBLREL. 01, LJ
LINOV-1996 (TREMBLREL. 01, LJ
LINOV-1996 (TREMBLREL. 01, LJ
DELTA-15 LINEOYL DESATURASE.
LIMNANTHES DOUGLASII.
EUKARYOTA; PLANTAE; EMBRYOBIC
POSIDAE; GERANIALES; LIMNANTE
                                                                                                                                                                                                                                 ₩
                                                                                                                                                                                                                                                                                                                                          109 NAKLNSVVGHILHSSILVPYNGW
                                                                                                                                                                                                                                                                                                                                                        TVAWYQV-SP-LAARLLYPYLAW
                                                                                                                                                                                                                                                      Similarity 28.9%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 8.5%;
Local Similarity 36.7%;
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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                                                                                                                                                                                                                                 380 AA;
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Best Local S
Matches 2
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SEQUENCE
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SEQUENCE
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Best Loc
Matches
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- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

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